

# SEQ SEARCH SUMMARY

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 12, 2003, 10:00:22 ; Search time 35.988 Seconds  
(without alignments)  
1975.923 Million cell updates/sec

Title: US-09-674-330A-3  
Perfect score: 2536  
Sequence: 1 MPGLKRILTVTILALWLPHP.....INFRGSSVIRLRIYVSQYPF 448

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_19Jun03:\*

1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:\*

2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:\*

3: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:\*

4: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:\*

5: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:\*

6: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:\*

7: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:\*

8: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:\*

9: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:\*

10: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:\*

11: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:\*

12: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:\*

13: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:\*

14: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:\*

15: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:\*

16: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:\*

17: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:\*

18: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:\*

19: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:\*

20: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:\*

21: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:\*

22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:\*

23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:\*

24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query Match	% Length	DB	ID	Description
1	2536	100.0	448	21	AAY56750	Smooth muscle prol
2	2536	100.0	448	21	AAY54990	Full length mouse
3	2505	98.8	461	21	AAY56752	Smooth muscle prol
4	2505	98.8	461	21	AAY54991	Full length mouse
5	2405	94.8	448	19	AAW79739	Human EGF protein
6	2405	94.8	448	20	AAW95709	Homo sapiens fetal
7	2405	94.8	448	20	AAW94281	Human extracellular
8	2405	94.8	448	21	AAY57058	Amino acid sequenc
9	2405	94.8	448	21	AAY54989	Full length human
10	2405	94.8	448	22	AAM93573	Human polypeptide,
11	2405	94.8	448	23	AAU75494	Human extracellular
12	2403	94.8	423	21	AAY56751	Smooth muscle prol
13	2403	94.8	423	21	AAY56753	Smooth muscle prol
14	2399	94.6	448	20	AAY08063	Human EGF-like hom
15	2399	94.6	448	22	AAU29227	Human PRO polypept
16	2399	94.6	448	22	AAB31183	Amino acid sequenc
17	2399	94.6	448	24	ABU71315	Human PRO210 prote
18	2399	94.6	448	24	ABU72040	Novel human secret
19	2399	94.6	448	24	ABU65772	Human secreted/tra
20	2399	94.6	448	24	ABU66105	Novel human secret
21	2399	94.6	448	24	ABU67141	Novel human secret
22	2399	94.6	448	24	ABU67272	Novel human secret
23	2399	94.6	448	24	ABU67609	Human secreted/tra
24	2399	94.6	448	24	ABU65467	Human PRO polypept
25	2399	94.6	448	24	ABU58603	Human PRO polypept
26	2399	94.6	448	24	ABU56139	Human secreted/tra
27	2399	94.6	448	24	ABU57134	Human PRO polypept
28	2399	94.6	448	24	ABU10713	Human secreted/tra
29	2125	83.8	392	18	AAW31705	Human extracellular
30	1869	73.7	335	21	AAY76008	Rat EGF extracellu
31	1869	73.7	335	22	AAB55947	Skin cell protein,
32	1869	73.7	335	23	ABB72147	Rat protein isolat
33	1275	50.3	443	18	AAW32110	Human extracellular
34	1275	50.3	443	20	AAY16587	Extracellular prot
35	1275	50.3	443	21	AAB33418	Human PRO226 prote
36	1275	50.3	443	21	AAY84707	A human p53 mutant
37	1275	50.3	443	21	AAY55850	Human S1-5 ECMP-li
38	1275	50.3	443	22	AAU12330	Human PRO226 polyp
39	1275	50.3	443	23	AAU86130	Human PRO226 polyp
40	1275	50.3	443	24	ABU66728	Human PRO polypept
41	1275	50.3	443	24	ABU67004	Human secreted/tra
42	1275	50.3	443	24	ABU59809	Novel secreted and
43	1271	50.1	443	22	AAB92533	Human protein sequ
44	1260	49.7	443	21	AAY84706	Amino acid sequenc
45	1225.5	48.3	433	21	AAB58353	Lung cancer associ

### ALIGNMENTS

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OM protein - protein search, using sw model

Run on: December 12, 2003, 10:01:28 ; Search time 15.1351 Seconds  
(without alignments)  
1252.401 Million cell updates/sec

Title: US-09-674-330A-3

Perfect score: 2536

Sequence: 1 MPGLKRILTVTILALWLPHP.....INFRGSSVIRLRIYVSQYPF 448

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA:\*

1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*

2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*

3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*

4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*

5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*

6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query			Description
		Match	Length	DB	
1	2405	94.8	448	2	US-08-884-072-1 Sequence 1, Appli
2	2405	94.8	448	4	US-09-212-168-1 Sequence 1, Appli
3	1869	73.7	335	4	US-09-312-283C-186 Sequence 186, App
4	1832	72.2	337	3	US-09-188-930-186 Sequence 186, App
5	1275	50.3	443	2	US-08-833-963C-2 Sequence 2, Appli
6	1275	50.3	443	3	US-08-980-514-1 Sequence 1, Appli
7	966.5	38.1	387	2	US-08-884-072-5 Sequence 5, Appli
8	966.5	38.1	387	2	US-08-833-963C-9 Sequence 9, Appli
9	966.5	38.1	387	3	US-08-980-514-3 Sequence 3, Appli
10	966.5	38.1	387	4	US-09-212-168-5 Sequence 5, Appli
11	897.5	35.4	274	3	US-09-188-930-336 Sequence 336, App

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OM protein - protein search, using sw model

Run on: December 12, 2003, 10:05:03 ; Search time 26.2342 Seconds  
(without alignments)  
3176.029 Million cell updates/sec

Title: US-09-674-330A-3

Perfect score: 2536

Sequence: 1 MPGLKRILTVTILALWLPHP.....INFRGSSVIRLRIYVSQYPF 448

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 684280 seqs, 185983659 residues

Total number of hits satisfying chosen parameters: 684280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:  
1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:  
6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:  
9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:  
10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:  
12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:  
13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:  
16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:  
17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:  
18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	2405	94.8	448	9	US-09-083-002-2	Sequence 2, Appli
2	2405	94.8	448	9	US-09-275-805-2	Sequence 2, Appli
3	2405	94.8	448	9	US-09-836-561-1	Sequence 1, Appli
4	2405	94.8	448	14	US-10-041-016-2	Sequence 2, Appli
5	2399	94.6	448	12	US-10-199-672-408	Sequence 408, App
6	2399	94.6	448	12	US-10-187-749-408	Sequence 408, App
7	2399	94.6	448	12	US-10-194-457-408	Sequence 408, App
8	2399	94.6	448	12	US-10-184-642-408	Sequence 408, App
9	2399	94.6	448	12	US-10-196-747-408	Sequence 408, App
10	2399	94.6	448	12	US-10-173-689-408	Sequence 408, App
11	2399	94.6	448	12	US-10-173-690-408	Sequence 408, App
12	2399	94.6	448	12	US-10-173-691-408	Sequence 408, App
13	2399	94.6	448	12	US-10-173-692-408	Sequence 408, App
14	2399	94.6	448	12	US-10-173-694-408	Sequence 408, App
15	2399	94.6	448	12	US-10-173-698-408	Sequence 408, App
16	2399	94.6	448	12	US-10-173-699-408	Sequence 408, App
17	2399	94.6	448	12	US-10-173-707-408	Sequence 408, App
18	2399	94.6	448	12	US-10-174-569-408	Sequence 408, App
19	2399	94.6	448	12	US-10-174-583-408	Sequence 408, App
20	2399	94.6	448	12	US-10-174-587-408	Sequence 408, App
21	2399	94.6	448	12	US-10-174-589-408	Sequence 408, App
22	2399	94.6	448	12	US-10-174-591-408	Sequence 408, App
23	2399	94.6	448	12	US-10-175-736-408	Sequence 408, App
24	2399	94.6	448	12	US-10-175-742-408	Sequence 408, App
25	2399	94.6	448	12	US-10-175-744-408	Sequence 408, App
26	2399	94.6	448	12	US-10-175-745-408	Sequence 408, App
27	2399	94.6	448	12	US-10-175-748-408	Sequence 408, App
28	2399	94.6	448	12	US-10-175-751-408	Sequence 408, App
29	2399	94.6	448	12	US-10-175-754-408	Sequence 408, App
30	2399	94.6	448	12	US-10-176-480-408	Sequence 408, App
31	2399	94.6	448	12	US-10-176-489-408	Sequence 408, App
32	2399	94.6	448	12	US-10-176-754-408	Sequence 408, App
33	2399	94.6	448	12	US-10-176-755-408	Sequence 408, App
34	2399	94.6	448	12	US-10-176-759-408	Sequence 408, App
35	2399	94.6	448	12	US-10-176-920-408	Sequence 408, App
36	2399	94.6	448	12	US-10-176-922-408	Sequence 408, App
37	2399	94.6	448	12	US-10-176-924-408	Sequence 408, App
38	2399	94.6	448	12	US-10-176-984-408	Sequence 408, App
39	2399	94.6	448	12	US-10-179-508-408	Sequence 408, App
40	2399	94.6	448	12	US-10-179-512-408	Sequence 408, App
41	2399	94.6	448	12	US-10-179-515-408	Sequence 408, App
42	2399	94.6	448	12	US-10-066-198-15	Sequence 15, Appl
43	2399	94.6	448	12	US-10-173-702-408	Sequence 408, App
44	2399	94.6	448	12	US-10-173-703-408	Sequence 408, App
45	2399	94.6	448	12	US-10-173-704-408	Sequence 408, App

## ALIGNMENTS

RESULT 1  
US-09-083-002-2

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OM protein - protein search, using sw model

Run on: December 12, 2003, 10:00:22 ; Search time 14.1261 Seconds  
(without alignments)  
3049.921 Million cell updates/sec

Title: US-09-674-330A-3

Perfect score: 2536

Sequence: 1 MPGLKRILTVTILALWLPHP.....INFRGSSVIRLRIYVSQYPF 448

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_76:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	1119.5	44.1	493	2	JC5621	epidermal growth f
2	966.5	38.1	387	2	I38449	extracellular prot
3	764.5	30.1	1221	2	A49457	fibulin-2 precurso
4	736.5	29.0	1184	2	A55184	fibulin-2 precurso
5	733.5	28.9	685	2	S78040	fibulin, splice fo
6	729.5	28.8	683	2	C36346	fibulin 1 precurso
7	688	27.1	705	2	S34968	fibulin, splice fo
8	613.5	24.2	601	2	B36346	fibulin 1 precurso
9	608	24.0	689	2	T42760	fibulin, splice fo
10	600	23.7	712	2	T42990	fibulin 1, splice
11	597.5	23.6	589	2	T43210	fibulin-1D precurs
12	573	22.6	798	2	T22793	hypothetical prote
13	537	21.2	1394	2	A35626	transforming growt

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### OM protein - protein search, using sw model

Run on: December 12, 2003, 10:00:22 ; Search time 9.08108 Seconds  
(without alignments)  
2319.984 Million cell updates/sec

Title: US-09-674-330A-3

Perfect score: 2536

Sequence: 1 MPGLKRILTVTILALWLPHP.....INFRGSSVIRLRIYVSQYPF 448

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt 41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Query						Score	Match	Length	DB	ID	Description
No.												
1	2536	100.0	448	1	FBL5_MOUSE							Q9wvh9 mus musculu
2	2500	98.6	448	1	FBL5_RAT							Q9wvh8 rattus norv
3	2405	94.8	448	1	FBL5_HUMAN							Q9ubx5 homo sapien
4	1275	50.3	443	1	FBL4_HUMAN							O95967 homo sapien
5	1269	50.0	443	1	FBL4_CRIGR							O55058 cricetus
6	1260	49.7	443	1	FBL4_MOUSE							Q9wj9 mus musculu
7	1119.5	44.1	493	1	FBL3_RAT							O35568 rattus norv
8	1104	43.5	493	1	FBL3_HUMAN							Q12805 homo sapien
9	764.5	30.1	1221	1	FBL2_MOUSE							P37889 mus musculu
10	736.5	29.0	1184	1	FBL2_HUMAN							P98095 homo sapien
11	722	28.5	704	1	FBL1_CHICK							O73775 gallus gall
12	711	28.0	598	1	FBL1_CERAE							Q8mj9 cercopithec
13	695	27.4	703	1	FBL1_HUMAN							P23142 homo sapien
14	685	27.0	705	1	FBL1_MOUSE							Q08879 mus musculu
15	654.5	25.8	681	1	FBL1_BRARE							O42182 brachydanio
16	573	22.6	798	1	FBL1_CAEEL							O77469 caenorhabdi
17	537	21.2	1394	1	LTBS_HUMAN							P22064 homo sapien

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OM protein - protein search, using sw model

Run on: December 12, 2003, 10:00:22 ; Search time 30.6066 Seconds  
(without alignments)  
3777.210 Million cell updates/sec

Title: US-09-674-330A-3

Perfect score: 2536

Sequence: 1 MPGLKRILTVTILALWLPHP.....INFRGSSVIRLRIYVSQYPF 448

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_23:  
1: sp\_archea:  
2: sp\_bacteria:  
3: sp\_fungi:  
4: sp\_human:  
5: sp\_invertebrate:  
6: sp\_mammal:  
7: sp\_mhc:  
8: sp\_organelle:  
9: sp\_phage:  
10: sp\_plant:  
11: sp\_rat:  
12: sp\_virus:  
13: sp\_vertebrate:  
14: sp\_unclassified:  
15: sp\_rvirus:  
16: sp\_bacteriap:  
17: sp\_archeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	1275	50.3	443	4	Q96TF5	Q96tf5 homo sapien
2	1261	49.7	443	11	Q9JM06	Q9jm06 mus musculu
3	1252	49.4	443	4	Q9H3D5	Q9h3d5 homo sapien
4	1109	43.7	493	11	Q8BPB5	Q8bpb5 mus musculu
5	967	38.1	387	11	Q8K0J4	Q8k0j4 mus musculu
6	767.5	30.3	1174	11	Q99K58	Q99k58 mus musculu
7	738.5	29.1	576	4	Q9Y3V7	Q9y3v7 homo sapien
8	737.5	29.1	1231	4	Q8IUI1	Q8iui1 homo sapien
9	736.5	29.0	1231	4	Q8IUI0	Q8iui0 homo sapien
10	730.5	28.8	685	11	Q922K8	Q922k8 mus musculu
11	730.5	28.8	685	11	Q8C3B1	Q8c3b1 mus musculu
12	729.5	28.8	683	4	Q8TBH8	Q8tbh8 homo sapien
13	722	28.5	704	13	O73774	O73774 gallus gall
14	711	28.0	598	6	Q8MJJ9	Q8mjj9 cercopithec
15	690	27.2	638	4	Q8NBH6	Q8nbh6 homo sapien
16	664.5	26.2	495	4	Q9HBQ5	Q9hbq5 homo sapien
17	654.5	25.8	681	13	O42182	O42182 brachydanio
18	620	24.4	698	5	Q9V4B8	Q9v4b8 drosophila
19	577.5	22.8	554	4	Q9UH16	Q9uh16 homo sapien
20	561	22.1	1409	5	Q9VS89	Q9vs89 drosophila
21	557	22.0	2673	4	Q96SC3	Q96sc3 homo sapien
22	546	21.5	5636	4	Q96RW7	Q96rw7 homo sapien
23	527.5	20.8	2872	11	Q9WUH8	Q9wuh8 rattus norv
24	527	20.8	3857	11	O88840	O88840 mus musculu
25	524.5	20.7	1398	13	Q8AXM6	Q8axm6 xenopus lae
26	524.5	20.7	1399	13	Q8JFZ4	Q8jfz4 xenopus lae
27	524.5	20.7	2809	4	Q96JP8	Q96jp8 homo sapien
28	520.5	20.5	741	4	Q96K89	Q96k89 homo sapien
29	515	20.3	1389	11	Q8CG18	Q8cg18 mus musculu
30	515	20.3	1713	11	Q8CG19	Q8cg19 mus musculu
31	514	20.3	188	11	Q8R1U8	Q8rlu8 mus musculu
32	513.5	20.2	2906	11	Q9WUH9	Q9wuh9 rattus norv
33	512.5	20.2	787	11	Q8K061	Q8k061 mus musculu
34	511	20.1	1713	11	O88349	O88349 mus musculu
35	509.5	20.1	708	13	P87363	P87363 gallus gall
36	503.5	19.9	937	5	Q9BLJ1	Q9blj1 ciona intes
37	495.5	19.5	729	11	Q8BNH3	Q8bnh3 mus musculu
38	492.5	19.4	746	4	Q96HB9	Q96hb9 homo sapien
39	492.5	19.4	893	6	Q8MJK0	Q8mjk0 cercopithec
40	492.5	19.4	1256	4	Q9NS15	Q9ns15 homo sapien
41	492.5	19.4	1382	4	Q9H7K2	Q9h7k2 homo sapien
42	492	19.4	1289	5	Q8SSS3	Q8sss3 dictyosteli
43	492	19.4	1963	6	Q28019	Q28019 bos taurus
44	489.5	19.3	1062	11	Q60789	Q60789 mus musculu
45	485.5	19.1	1764	11	O35806	O35806 rattus norv

## ALIGNMENTS

RESULT 1  
Q96TF5

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OM protein - protein search, using sw model

Run on: December 12, 2003, 10:00:22 ; Search time 37.0323 Seconds  
(without alignments)  
1975.923 Million cell updates/sec

Title: US-09-674-330A-8  
Perfect score: 2610  
Sequence: 1 MGPRSFEPMHSGLCRQRRMI.....INFRGSSVIRLRIYVSQYPF 461

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_19Jun03:\*

1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:\*

2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:\*

3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:\*

4: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:\*

5: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:\*

6: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:\*

7: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:\*

8: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:\*

9: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:\*

10: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:\*

11: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:\*

12: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:\*

13: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:\*

14: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:\*

15: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT:\*

16: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:\*

17: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT:\*

18: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:\*

19: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:\*

20: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:\*

21: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:\*

22: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:\*

23: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:\*

24: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2610	100.0	461	21	AAY56752	Smooth muscle prol
2	2610	100.0	461	21	AAY54991	Full length mouse
3	2505	96.0	448	21	AAY56750	Smooth muscle prol
4	2505	96.0	448	21	AAY54990	Full length mouse
5	2403	92.1	423	21	AAY56751	Smooth muscle prol
6	2403	92.1	423	21	AAY56753	Smooth muscle prol
7	2376	91.0	448	19	AAW79739	Human EGF protein
8	2376	91.0	448	20	AAW95709	Homo sapiens fetal
9	2376	91.0	448	20	AAW94281	Human extracellular
10	2376	91.0	448	21	AAY57058	Amino acid sequenc
11	2376	91.0	448	21	AAY54989	Full length human
12	2376	91.0	448	22	AAM93573	Human polypeptide,
13	2376	91.0	448	23	AAU75494	Human extracellular
14	2370	90.8	448	20	AAY08063	Human EGF-like hom
15	2370	90.8	448	22	AAU29227	Human PRO polypept
16	2370	90.8	448	22	AAB31183	Amino acid sequenc
17	2370	90.8	448	24	ABU71315	Human PRO210 prote
18	2370	90.8	448	24	ABU72040	Novel human secret
19	2370	90.8	448	24	ABU65772	Human secreted/tra
20	2370	90.8	448	24	ABU66105	Novel human secret
21	2370	90.8	448	24	ABU67141	Novel human secret
22	2370	90.8	448	24	ABU67272	Novel human secret
23	2370	90.8	448	24	ABU67609	Human secreted/tra
24	2370	90.8	448	24	ABU65467	Human PRO polypept
25	2370	90.8	448	24	ABU58603	Human PRO polypept
26	2370	90.8	448	24	ABU56139	Human secreted/tra
27	2370	90.8	448	24	ABU57134	Human PRO polypept
28	2370	90.8	448	24	ABU10713	Human secreted/tra
29	2125	81.4	392	18	AAW31705	Human extracellular
30	1869	71.6	335	21	AAY76008	Rat EGF extracellu
31	1869	71.6	335	22	AAB55947	Skin cell protein,
32	1869	71.6	335	23	ABB72147	Rat protein isolat
33	1268	48.6	443	18	AAW32110	Human extracellular
34	1268	48.6	443	20	AAY16587	Extracellular prot
35	1268	48.6	443	21	AAB33418	Human PRO226 prote
36	1268	48.6	443	21	AAY84707	A human p53 mutant
37	1268	48.6	443	21	AAY55850	Human S1-5 ECMP-li
38	1268	48.6	443	22	AAU12330	Human PRO226 polyp
39	1268	48.6	443	23	AAU86130	Human PRO226 polyp
40	1268	48.6	443	24	ABU66728	Human PRO polypept
41	1268	48.6	443	24	ABU67004	Human secreted/tra
42	1268	48.6	443	24	ABU59809	Novel secreted and
43	1264	48.4	443	22	AAB92533	Human protein sequ
44	1257	48.2	443	21	AAY84706	Amino acid sequenc
45	1225.5	47.0	433	21	AAB58353	Lung cancer associ

### ALIGNMENTS

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OM protein - protein search, using sw model

Run on: December 12, 2003, 10:01:28 ; Search time 15.5743 Seconds  
(without alignments)  
1252.401 Million cell updates/sec

Title: US-09-674-330A-8

Perfect score: 2610

Sequence: 1 MGPRSFEPMHSGLCRQRRMI.....INFRGSSVIRLRIYVSQYPP 461

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA:\*

1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*

2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*

3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*

4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*

5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*

6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query			Description
		Match	Length	DB	ID
<hr/>					
1	2376	91.0	448	2	US-08-884-072-1
2	2376	91.0	448	4	US-09-212-168-1
3	1869	71.6	335	4	US-09-312-283C-186
4	1832	70.2	337	3	US-09-188-930-186
5	1268	48.6	443	2	US-08-833-963C-2
6	1268	48.6	443	3	US-08-980-514-1
7	966.5	37.0	387	2	US-08-884-072-5
8	966.5	37.0	387	2	US-08-833-963C-9
9	966.5	37.0	387	3	US-08-980-514-3
10	966.5	37.0	387	4	US-09-212-168-5
11	897.5	34.4	274	3	US-09-188-930-336

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OM protein - protein search, using sw model

Run on: December 12, 2003, 10:05:03 ; Search time 26.9955 Seconds  
(without alignments)  
3176.029 Million cell updates/sec

Title: US-09-674-330A-8

Perfect score: 2610

Sequence: 1 MGPRSFEPMHSGLCRQRRMID.....INFRGSSVIRLRIYVSQYPF 461

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 684280 seqs, 185983659 residues

Total number of hits satisfying chosen parameters: 684280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA:  
1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*

2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*

3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*

4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*

5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*

6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*

7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*

8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*

9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*

10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*

11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*

12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*

13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*

14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*

15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*

16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*

17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*

18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	2376	91.0	448	9	US-09-083-002-2	Sequence 2, Appli
2	2376	91.0	448	9	US-09-275-805-2	Sequence 2, Appli
3	2376	91.0	448	9	US-09-836-561-1	Sequence 1, Appli
4	2376	91.0	448	14	US-10-041-016-2	Sequence 2, Appli
5	2370	90.8	448	12	US-10-199-672-408	Sequence 408, App
6	2370	90.8	448	12	US-10-187-749-408	Sequence 408, App
7	2370	90.8	448	12	US-10-194-457-408	Sequence 408, App
8	2370	90.8	448	12	US-10-184-642-408	Sequence 408, App
9	2370	90.8	448	12	US-10-196-747-408	Sequence 408, App
10	2370	90.8	448	12	US-10-173-689-408	Sequence 408, App
11	2370	90.8	448	12	US-10-173-690-408	Sequence 408, App
12	2370	90.8	448	12	US-10-173-691-408	Sequence 408, App
13	2370	90.8	448	12	US-10-173-692-408	Sequence 408, App
14	2370	90.8	448	12	US-10-173-694-408	Sequence 408, App
15	2370	90.8	448	12	US-10-173-698-408	Sequence 408, App
16	2370	90.8	448	12	US-10-173-699-408	Sequence 408, App
17	2370	90.8	448	12	US-10-173-707-408	Sequence 408, App
18	2370	90.8	448	12	US-10-174-569-408	Sequence 408, App
19	2370	90.8	448	12	US-10-174-583-408	Sequence 408, App
20	2370	90.8	448	12	US-10-174-587-408	Sequence 408, App
21	2370	90.8	448	12	US-10-174-589-408	Sequence 408, App
22	2370	90.8	448	12	US-10-174-591-408	Sequence 408, App
23	2370	90.8	448	12	US-10-175-736-408	Sequence 408, App
24	2370	90.8	448	12	US-10-175-742-408	Sequénce 408, App
25	2370	90.8	448	12	US-10-175-744-408	Sequence 408, App
26	2370	90.8	448	12	US-10-175-745-408	Sequence 408, App
27	2370	90.8	448	12	US-10-175-748-408	Sequence 408, App
28	2370	90.8	448	12	US-10-175-751-408	Sequence 408, App
29	2370	90.8	448	12	US-10-175-754-408	Sequence 408, App
30	2370	90.8	448	12	US-10-176-480-408	Sequence 408, App
31	2370	90.8	448	12	US-10-176-489-408	Sequence 408, App
32	2370	90.8	448	12	US-10-176-754-408	Sequence 408, App
33	2370	90.8	448	12	US-10-176-755-408	Sequence 408, App
34	2370	90.8	448	12	US-10-176-759-408	Sequence 408, App
35	2370	90.8	448	12	US-10-176-920-408	Sequence 408, App
36	2370	90.8	448	12	US-10-176-922-408	Sequence 408, App
37	2370	90.8	448	12	US-10-176-924-408	Sequence 408, App
38	2370	90.8	448	12	US-10-176-984-408	Sequence 408, App
39	2370	90.8	448	12	US-10-179-508-408	Sequence 408, App
40	2370	90.8	448	12	US-10-179-512-408	Sequence 408, App
41	2370	90.8	448	12	US-10-179-515-408	Sequence 408, App
42	2370	90.8	448	12	US-10-066-198-15	Sequence 15, Appl
43	2370	90.8	448	12	US-10-173-702-408	Sequence 408, App
44	2370	90.8	448	12	US-10-173-703-408	Sequence 408, App
45	2370	90.8	448	12	US-10-173-704-408	Sequence 408, App

## ALIGNMENTS

RESULT 1  
US-09-083-002-2

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OM protein - protein search, using sw model

Run on: December 12, 2003, 10:00:22 ; Search time 14.536 Seconds  
(without alignments)  
3049.921 Million cell updates/sec

Title: US-09-674-330A-8

Perfect score: 2610

Sequence: 1 MGPRSFEPMHSGLCRQRRMI.....INFRGSSVIRLRIYVSQYPF 461

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_76:  
1: pir1:  
2: pir2:  
3: pir3:  
4: pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Query	% No. Score Match Length DB ID				Description
1	PIR_76:*	1	pir1:*			
2	PIR_76:*	1	pir2:*			
3	PIR_76:*	1	pir3:*			
4	PIR_76:*	1	pir4:*			
-----	-----	-----	-----	-----	-----	-----
1	epidermal growth f	1119.5	42.9	493	2	JC5621
2	extracellular prot	966.5	37.0	387	2	I38449
3	fibulin-2 precurso	764.5	29.3	1221	2	A49457
4	fibulin-2 precurso	736.5	28.2	1184	2	A55184
5	fibulin, splice fo	733.5	28.1	685	2	S78040
6	fibulin 1 precurso	729.5	28.0	683	2	C36346
7	fibulin, splice fo	688	26.4	705	2	S34968
8	fibulin 1 precurso	613.5	23.5	601	2	B36346
9	fibulin, splice fo	608	23.3	689	2	T42760
10	fibulin 1, splice	600	23.0	712	2	T42990
11	fibulin-1D precurs	597.5	22.9	589	2	T43210
12	hypothetical prote	573	22.0	798	2	T22793
13	transforming growt	537	20.6	1394	2	A35626

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OM protein - protein search, using sw model

Run on: December 12, 2003, 10:00:22 ; Search time 9.34459 Seconds  
(without alignments)  
2319.984 Million cell updates/sec

Title: US-09-674-330A-8

Perfect score: 2610

Sequence: 1 MGPRSFEPMHSGLCRQRRM.....INFRGSSVIRLRIYVSQYPF 461

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Query						
No.	Score	Match	Length	DB	ID	Description	
1	2505	96.0	448	1	FBL5_MOUSE	LATE	Q9wvh9 mus musculu 1999 ART
2	2469	94.6	448	1	FBL5_RAT		Q9wvh8 rattus norv
3	2376	91.0	448	1	FBL5_HUMAN		Q9ubx5 homo sapien
4	1268	48.6	443	1	FBL4_HUMAN		Q95967 homo sapien
5	1262	48.4	443	1	FBL4_CRIGR		Q55058 cricetus
6	1257	48.2	443	1	FBL4_MOUSE		Q9wj9 mus musculu
7	1119.5	42.9	493	1	FBL3_RAT		Q35568 rattus norv
8	1103	42.3	493	1	FBL3_HUMAN		Q12805 homo sapien
9	764.5	29.3	1221	1	FBL2_MOUSE		P37889 mus musculu
10	736.5	28.2	1184	1	FBL2_HUMAN		P98095 homo sapien
11	722	27.7	704	1	FBL1_CHICK		Q73775 gallus gall
12	711	27.2	598	1	FBL1_CERAE		Q8mjj9 cercopithec
13	695	26.6	703	1	FBL1_HUMAN		P23142 homo sapien
14	685	26.2	705	1	FBL1_MOUSE		Q08879 mus musculu
15	654.5	25.1	681	1	FBL1_BRARE		Q42182 brachydanio
16	573	22.0	798	1	FBL1_CAEEL		Q77469 caenorhabdi
17	537	20.6	1394	1	LTBS_HUMAN		P22064 homo sapien

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OM protein - protein search, using sw model

Run on: December 12, 2003, 10:00:22 ; Search time 31.4947 Seconds  
(without alignments)  
3777.210 Million cell updates/sec

Title: US-09-674-330A-8

Perfect score: 2610

Sequence: 1 MGPRSFEPMHSGLCRQRRMI.....INFRGSSVIRLRIYVSQYPF 461

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL\_23:  
1: sp\_archea:  
2: sp\_bacteria:  
3: sp\_fungi:  
4: sp\_human:  
5: sp\_invertebrate:  
6: sp\_mammal:  
7: sp\_mhc:  
8: sp\_organelle:  
9: sp\_phage:  
10: sp\_plant:  
11: sp\_rat:  
12: sp\_virus:  
13: sp\_vertebrate:  
14: sp\_unclassified:  
15: sp\_rvirus:  
16: sp\_bacteriap:  
17: sp\_archeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	1268	48.6	443	4	Q96TF5	Q96tf5 homo sapien
2	1258	48.2	443	11	Q9JM06	Q9jm06 mus musculu
3	1245	47.7	443	4	Q9H3D5	Q9h3d5 homo sapien
4	1109	42.5	493	11	Q8BPB5	Q8bpb5 mus musculu
5	967	37.0	387	11	Q8K0J4	Q8k0j4 mus musculu
6	767.5	29.4	1174	11	Q99K58	Q99k58 mus musculu
7	738.5	28.3	576	4	Q9Y3V7	Q9y3v7 homo sapien
8	737.5	28.3	1231	4	Q8IUI1	Q8iui1 homo sapien
9	736.5	28.2	1231	4	Q8IUI0	Q8iui0 homo sapien
10	730.5	28.0	685	11	Q922K8	Q922k8 mus musculu
11	730.5	28.0	685	11	Q8C3B1	Q8c3b1 mus musculu
12	729.5	28.0	683	4	Q8TBH8	Q8tbh8 homo sapien
13	722	27.7	704	13	Q73774	Q73774 gallus gall
14	711	27.2	598	6	Q8MJJ9	Q8mjj9 cercopithec
15	690	26.4	638	4	Q8NBH6	Q8nbh6 homo sapien
16	664.5	25.5	495	4	Q9HBQ5	Q9hbq5 homo sapien
17	654.5	25.1	681	13	O42182	O42182 brachydanio
18	620	23.8	698	5	Q9V4B8	Q9v4b8 drosophila
19	577.5	22.1	554	4	Q9UH16	Q9uh16 homo sapien
20	561	21.5	1409	5	Q9VS89	Q9vs89 drosophila
21	557	21.3	2673	4	Q96SC3	Q96sc3 homo sapien
22	546	20.9	5636	4	Q96RW7	Q96rw7 homo sapien
23	527.5	20.2	2872	11	Q9WUH8	Q9wuh8 rattus norv
24	527	20.2	3857	11	O88840	O88840 mus musculu
25	526.5	20.2	2809	4	Q96JP8	Q96jp8 homo sapien
26	524.5	20.1	1398	13	Q8AXM6	Q8axm6 xenopus lae
27	524.5	20.1	1399	13	Q8JFZ4	Q8jfz4 xenopus lae
28	520.5	19.9	741	4	Q96K89	Q96k89 homo sapien
29	515	19.7	1389	11	Q8CG18	Q8cg18 mus musculu
30	515	19.7	1713	11	Q8CG19	Q8cg19 mus musculu
31	514.5	19.7	2906	11	Q9WUH9	Q9wuh9 rattus norv
32	514	19.7	188	11	Q8R1U8	Q8r1u8 mus musculu
33	513	19.7	787	11	Q8K061	Q8k061 mus musculu
34	511	19.6	1713	11	O88349	O88349 mus musculu
35	509.5	19.5	708	13	P87363	P87363 gallus gall
36	503.5	19.3	937	5	Q9BLJ1	Q9bjl1 ciona intes
37	496	19.0	729	11	Q8BNH3	Q8bnh3 mus musculu
38	495	19.0	1963	6	Q28019	Q28019 bos taurus
39	492.5	18.9	746	4	Q96HB9	Q96hb9 homo sapien
40	492.5	18.9	893	6	Q8MJK0	Q8mjk0 cercopithec
41	492.5	18.9	1256	4	Q9NS15	Q9ns15 homo sapien
42	492.5	18.9	1382	4	Q9H7K2	Q9h7k2 homo sapien
43	492	18.9	1289	5	Q8SSS3	Q8sss3 dictyosteli
44	492	18.9	1764	11	O35806	O35806 rattus norv
45	489.5	18.8	1062	11	Q60789	Q60789 mus musculu

## ALIGNMENTS

RESULT 1  
Q96TF5

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OM protein - protein search, using sw model

Run on: December 12, 2003, 10:00:22 ; Search time 33.9797 Seconds  
(without alignments)  
1975.923 Million cell updates/sec

Title: US-09-674-330A-9

Perfect score: 2403

Sequence: 1 QCTNGFDLDRQSGQCLDIDE.....INFRGSSVIRLRIYVSQYPF 423

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_19Jun03:\*

1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:\*

2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:\*

3: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:\*

4: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:\*

5: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:\*

6: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:\*

7: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:\*

8: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:\*

9: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:\*

10: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:\*

11: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:\*

12: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:\*

13: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:\*

14: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:\*

15: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:\*

16: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:\*

17: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:\*

18: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:\*

19: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:\*

20: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:\*

21: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:\*

22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:\*

23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:\*

24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2403	100.0	423	21	AAY56751	Smooth muscle prol
2	2403	100.0	423	21	AAY56753	Smooth muscle prol
3	2403	100.0	448	21	AAY56750	Smooth muscle prol
4	2403	100.0	448	21	AAY54990	Full length mouse
5	2403	100.0	461	21	AAY56752	Smooth muscle prol
6	2403	100.0	461	21	AAY54991	Full length mouse
7	2302	95.8	448	19	AAW79739	- HUMAN
8	2302	95.8	448	20	AAW95709	Human EGF protein
9	2302	95.8	448	20	AAW94281	Homo sapiens fetal
10	2302	95.8	448	21	AAY57058	Human extracellula
11	2302	95.8	448	21	AAY54989	Amino acid sequenc
12	2302	95.8	448	22	AAM93573	Full length human
13	2302	95.8	448	23	AAU75494	Human polypeptide,
14	2296	95.5	448	20	AAY08063	Human extracellula
15	2296	95.5	448	22	AAU29227	Human EGF-like hom
16	2296	95.5	448	22	AAB31183	Human PRO polypept
17	2296	95.5	448	24	ABU71315	Amino acid sequenc
18	2296	95.5	448	24	ABU72040	Human PRO210 prote
19	2296	95.5	448	24	ABU65772	Novel human secret
20	2296	95.5	448	24	ABU66105	Human secreted/tra
21	2296	95.5	448	24	ABU67141	Novel human secret
22	2296	95.5	448	24	ABU67272	Novel human secret
23	2296	95.5	448	24	ABU67609	Novel human secret
24	2296	95.5	448	24	ABU65467	Human secreted/tra
25	2296	95.5	448	24	ABU58603	Human PRO polypept
26	2296	95.5	448	24	ABU56139	Human secreted/tra
27	2296	95.5	448	24	ABU57134	Human PRO polypept
28	2296	95.5	448	24	ABU10713	Human secreted/tra
29	2125	88.4	392	18	AAW31705	Human extracellula
30	1869	77.8	335	21	AAY76008	Rat EGF extracellu
31	1869	77.8	335	22	AAB55947	Skin cell protein,
32	1869	77.8	335	23	ABB72147	Rat protein isolat
33	1264.5	52.6	443	18	AAW32110	Human extracellula
34	1264.5	52.6	443	20	AAY16587	Extracellular prot
35	1264.5	52.6	443	21	AAB33418	Human PRO226 prote
36	1264.5	52.6	443	21	AAY84707	A human p53 mutant
37	1264.5	52.6	443	21	AAY55850	Human S1-5. ECMP-li
38	1264.5	52.6	443	22	AAU12330	Human PRO226 polyp
39	1264.5	52.6	443	23	AAU86130	Human PRO226 polyp
40	1264.5	52.6	443	24	ABU66728	Human PRO polypept
41	1264.5	52.6	443	24	ABU67004	Human secreted/tra
42	1264.5	52.6	443	24	ABU59809	Novel secreted and
43	1260.5	52.5	443	22	AAB92533	Human protein sequ
44	1252.5	52.1	443	21	AAY84706	Amino acid sequenc
45	1225.5	51.0	433	21	AAB58353	Lung cancer associ

### ALIGNMENTS

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OM protein - protein search, using sw model

Run on: December 12, 2003, 10:01:28 ; Search time 14.2905 Seconds  
(without alignments)  
1252.401 Million cell updates/sec

Title: US-09-674-330A-9

Perfect score: 2403

Sequence: 1 QCTNGFDLDRQSGQCLDIDE.....INFRGSSVIRLRIYVSQYPF 423

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA:\*

1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*

2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*

3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*

4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*

5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*

6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

%

Result	Query				Description
No.	Score	Match	Length	DB	ID
1	2302	95.8	448	2	US-08-884-072-1 >human
2	2302	95.8	448	4	US-09-212-168-1
3	1869	77.8	335	4	US-09-312-283C-186
4	1832	76.2	337	3	US-09-188-930-186
5	1264.5	52.6	443	2	US-08-833-963C-2
6	1264.5	52.6	443	3	US-08-980-514-1
7	966.5	40.2	387	2	US-08-884-072-5
8	966.5	40.2	387	2	US-08-833-963C-9
9	966.5	40.2	387	3	US-08-980-514-3
10	966.5	40.2	387	4	US-09-212-168-5
11	897.5	37.3	274	3	US-09-188-930-336

94.87

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OM protein - protein search, using sw model

Run on: December 12, 2003; 10:05:03 ; Search time 24.7703 Seconds  
(without alignments)  
3176.029 Million cell updates/sec

Title: US-09-674-330A-9

Perfect score: 2403

Sequence: 1 QCTNGFDLDRQSGQCLDIDE.....INFRGSSVIRLRIYVSQYPF 423

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 684280 seqs, 185983659 residues

Total number of hits satisfying chosen parameters: 684280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published\_Applications\_AA:\*

1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*

2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*

3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*

4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*

5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*

6: /cgn2\_6/ptodata/2/pubpaa/PCTU\$\_PUBCOMB.pep:\*

7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*

8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*

9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*

10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*

11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*

12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*

13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*

14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*

15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*

16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*

17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*

18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	2302	95.8	448	9	US-09-083-002-2	Sequence 2, Appli
2	2302	95.8	448	9	US-09-275-805-2	Sequence 2, Appli
3	2302	95.8	448	9	US-09-836-561-1	Sequence 1, Appli
4	2302	95.8	448	14	US-10-041-016-2	Sequence 2, Appli
5	2296	95.5	448	12	US-10-199-672-408	Sequence 408, App
6	2296	95.5	448	12	US-10-187-749-408	Sequence 408, App
7	2296	95.5	448	12	US-10-194-457-408	Sequence 408, App
8	2296	95.5	448	12	US-10-184-642-408	Sequence 408, App
9	2296	95.5	448	12	US-10-196-747-408	Sequence 408, App
10	2296	95.5	448	12	US-10-173-689-408	Sequence 408, App
11	2296	95.5	448	12	US-10-173-690-408	Sequence 408, App
12	2296	95.5	448	12	US-10-173-691-408	Sequence 408, App
13	2296	95.5	448	12	US-10-173-692-408	Sequence 408, App
14	2296	95.5	448	12	US-10-173-694-408	Sequence 408, App
15	2296	95.5	448	12	US-10-173-698-408	Sequence 408, App
16	2296	95.5	448	12	US-10-173-699-408	Sequence 408, App
17	2296	95.5	448	12	US-10-173-707-408	Sequence 408, App
18	2296	95.5	448	12	US-10-174-569-408	Sequence 408, App
19	2296	95.5	448	12	US-10-174-583-408	Sequence 408, App
20	2296	95.5	448	12	US-10-174-587-408	Sequence 408, App
21	2296	95.5	448	12	US-10-174-589-408	Sequence 408, App
22	2296	95.5	448	12	US-10-174-591-408	Sequence 408, App
23	2296	95.5	448	12	US-10-175-736-408	Sequence 408, App
24	2296	95.5	448	12	US-10-175-742-408	Sequence 408, App
25	2296	95.5	448	12	US-10-175-744-408	Sequence 408, App
26	2296	95.5	448	12	US-10-175-745-408	Sequence 408, App
27	2296	95.5	448	12	US-10-175-748-408	Sequence 408, App
28	2296	95.5	448	12	US-10-175-751-408	Sequence 408, App
29	2296	95.5	448	12	US-10-175-754-408	Sequence 408, App
30	2296	95.5	448	12	US-10-176-480-408	Sequence 408, App
31	2296	95.5	448	12	US-10-176-489-408	Sequence 408, App
32	2296	95.5	448	12	US-10-176-754-408	Sequence 408, App
33	2296	95.5	448	12	US-10-176-755-408	Sequence 408, App
34	2296	95.5	448	12	US-10-176-759-408	Sequence 408, App
35	2296	95.5	448	12	US-10-176-920-408	Sequence 408, App
36	2296	95.5	448	12	US-10-176-922-408	Sequence 408, App
37	2296	95.5	448	12	US-10-176-924-408	Sequence 408, App
38	2296	95.5	448	12	US-10-176-984-408	Sequence 408, App
39	2296	95.5	448	12	US-10-179-508-408	Sequence 408, App
40	2296	95.5	448	12	US-10-179-512-408	Sequence 408, App
41	2296	95.5	448	12	US-10-179-515-408	Sequence 408, App
42	2296	95.5	448	12	US-10-066-198-15	Sequence 15, Appl
43	2296	95.5	448	12	US-10-173-702-408	Sequence 408, App
44	2296	95.5	448	12	US-10-173-703-408	Sequence 408, App
45	2296	95.5	448	12	US-10-173-704-408	Sequence 408, App

## ALIGNMENTS

RESULT 1  
US-09-083-002-2

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OM protein - protein search, using sw model

Run on: December 12, 2003, 10:00:22 ; Search time 13.3378 Seconds  
(without alignments)  
3049.921 Million cell updates/sec

Title: US-09-674-330A-9

Perfect score: 2403

Sequence: 1 QCTNGFDLDRQSGQCLDIDE.....INFRGSSVIRLRIYVSQYPP 423

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_76:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	1118.5	46.5	493	2	JC5621	epidermal growth f
2	966.5	40.2	387	2	I38449	extracellular prot
3	754.5	31.4	1221	2	A49457	fibulin-2 precurs
4	733.5	30.5	685	2	S78040	fibulin, splice fo
5	729.5	30.4	683	2	C36346	fibulin 1 precurs
6	726.5	30.2	1184	2	A55184	fibulin-2 precurs
7	688	28.6	705	2	S34968	fibulin, splice fo
8	613.5	25.5	601	2	B36346	fibulin 1 precurs
9	608	25.3	689	2	T42760	fibulin, splice fo
10	600	25.0	712	2	T42990	fibulin 1, splice
11	597.5	24.9	589	2	T43210	fibulin-1D precurs
12	573	23.8	798	2	T22793	hypothetical prote
13	537	22.3	1394	2	A35626	transforming growt

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OM protein - protein search, using sw model

Run on: December 12, 2003, 10:00:22 ; Search time 8.57432 Seconds  
(without alignments)  
2319.984 Million cell updates/sec

Title: US-09-674-330A-9

Perfect score: 2403

Sequence: 1 QCTNGFDLDRQSGQCLDIDE.....INFRGSSVIRLRIYVSQYPF 423

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query				%	Description
No.	Score	Match	Length	DB	ID	
1	2403	100.0	448	1	FBL5_MOUSE	Q9wvh9 mus musculu
2	2367	98.5	448	1	FBL5_RAT	Q9wvh8 rattus norv
3	2302	95.8	448	1	FBL5_HUMAN	Q9ubx5 homo sapien
4	1264.5	52.6	443	1	FBL4_HUMAN	095967 homo sapien
5	1257.5	52.3	443	1	FBL4_CRIGR	055058 cricetus
6	1252.5	52.1	443	1	FBL4_MOUSE	Q9wj9 mus musculu
7	1118.5	46.5	493	1	FBL3_RAT	035568 rattus norv
8	1098.5	45.7	493	1	FBL3_HUMAN	Q12805 homo sapien
9	754.5	31.4	1221	1	FBL2_MOUSE	P37889 mus musculu
10	726.5	30.2	1184	1	FBL2_HUMAN	P98095 homo sapien
11	722	30.0	704	1	FBL1_CHICK	073775 gallus gall
12	711	29.6	598	1	FBL1_CERAE	Q8mjj9 cercopithec
13	695	28.9	703	1	FBL1_HUMAN	P23142 homo sapien
14	685	28.5	705	1	FBL1_MOUSE	Q08879 mus musculu
15	653.5	27.2	681	1	FBL1_BRARE	042182 brachydanio
16	573	23.8	798	1	FBL1_CAEEL	077469 caenorhabdi
17	537	22.3	1394	1	LTBS_HUMAN	P22064 homo sapien

Nakamura

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OM protein - protein search, using sw model

Run on: December 12, 2003, 10:00:22 ; Search time 28.8986 Seconds  
(without alignments)  
3777.210 Million cell updates/sec

Title: US-09-674-330A-9

Perfect score: 2403

Sequence: 1 QCTNGFDLDRQSGQCLDIDE.....INFRGSSVIRLRIYVSQYPF 423

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL\_23:\*

- 1: sp\_archea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rat:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	1264.5	52.6	443	4	Q96TF5	Q96tf5 homo sapien
2	1253.5	52.2	443	11	Q9JM06	Q9jm06 mus musculu
3	1241.5	51.7	443	4	Q9H3D5	Q9h3d5 homo sapien
4	1107.5	46.1	493	11	Q8Bpb5	Q8bpb5 mus musculu
5	967	40.2	387	11	Q8K0J4	Q8k0j4 mus musculu
6	757.5	31.5	1174	11	Q99K58	Q99k58 mus musculu
7	730.5	30.4	685	11	Q922K8	Q922k8 mus musculu
8	730.5	30.4	685	11	Q8C3B1	Q8c3b1 mus musculu
9	729.5	30.4	683	4	Q8TBH8	Q8tbh8 homo sapien
10	728.5	30.3	576	4	Q9Y3V7	Q9y3v7 homo sapien
11	727.5	30.3	1231	4	Q8IUI1	Q8iui1 homo sapien
12	726.5	30.2	1231	4	Q8IUI0	Q8iui0 homo sapien
13	722	30.0	704	13	Q73774	Q73774 gallus gall
14	711	29.6	598	6	Q8MJJ9	Q8mjj9 cercopithec
15	690	28.7	638	4	Q8NBH6	Q8nbh6 homo sapien
16	664.5	27.7	495	4	Q9HBQ5	Q9hbq5 homo sapien
17	653.5	27.2	681	13	O42182	O42182 brachydanio
18	615	25.6	698	5	Q9V4B8	Q9v4b8 drosophila
19	577.5	24.0	554	4	Q9UH16	Q9uh16 homo sapien
20	557	23.2	2673	4	Q96SC3	Q96sc3 homo sapien
21	554.5	23.1	1409	5	Q9VS89	Q9vs89 drosophila
22	546	22.7	5636	4	Q96RW7	Q96rw7 homo sapien
23	524.5	21.8	1398	13	Q8AXM6	Q8axm6 xenopus lae
24	524.5	21.8	1399	13	Q8JFZ4	Q8jfz4 xenopus lae
25	524.5	21.8	2872	11	Q9WUH8	Q9wuh8 rattus norv
26	524	21.8	3857	11	Q88840	Q88840 mus musculu
27	523.5	21.8	2809	4	Q96JP8	Q96jp8 homo sapien
28	515.5	21.5	741	4	Q96K89	Q96k89 homo sapien
29	515	21.4	1389	11	Q8CG18	Q8cg18 mus musculu
30	515	21.4	1713	11	Q8CG19	Q8cg19 mus musculu
31	514	21.4	188	11	Q8R1U8	Q8r1u8 mus musculu
32	511	21.3	1713	11	Q88349	Q88349 mus musculu
33	510.5	21.2	2906	11	Q9WUH9	Q9wuh9 rattus norv
34	506.5	21.1	708	13	P87363	P87363 gallus gall
35	504	21.0	787	11	Q8K061	Q8k061 mus musculu
36	495.5	20.6	937	5	Q9BLJ1	Q9blj1 ciona intes
37	490	20.4	1963	6	Q28019	Q28019 bos taurus
38	486.5	20.2	729	11	Q8BNH3	Q8bnh3 mus musculu
39	485.5	20.2	746	4	Q96HB9	Q96hb9 homo sapien
40	485.5	20.2	893	6	Q8MJK0	Q8mjk0 cercopithec
41	485.5	20.2	1256	4	Q9NS15	Q9ns15 homo sapien
42	485.5	20.2	1382	4	Q9H7K2	Q9h7k2 homo sapien
43	484.5	20.2	517	4	Q9NP01	Q9np01 homo sapien
44	483.5	20.1	1764	11	O35806	O35806 rattus norv
45	482	20.1	1289	5	Q8SSS3	Q8sss3 dictyosteli

## ALIGNMENTS

RESULT 1

Q96TF5

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OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 07:36:19 ; Search time 4857.03 Seconds  
(without alignments)  
11320.190 Million cell updates/sec

Title: US-09-674-330A-1

Perfect score: 1344

Sequence: 1 atgccaggattaaaaaggat.....atgtgtcgcatatccgttc 1344

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:  
1: gb\_ba:  
2: gb\_htg:  
3: gb\_in:  
4: gb\_om:  
5: gb\_ov:  
6: gb\_pat:  
7: gb\_ph:  
8: gb\_pl:  
9: gb\_pr:  
10: gb\_ro:  
11: gb\_sts:  
12: gb\_sy:  
13: gb\_un:  
14: gb\_vi:  
15: em\_ba:  
16: em\_fun:  
17: em\_hum:  
18: em\_in:  
19: em\_mu:  
20: em\_om:  
21: em\_or:  
22: em\_ov:  
23: em\_pat:  
24: em\_ph:  
25: em\_pl:  
26: em\_ro:  
27: em\_sts:

28: em\_un:\*
   
 29: em\_vi:\*
   
 30: em\_htg\_hum:\*
   
 31: em\_htg\_inv:\*
   
 32: em\_htg\_other:\*
   
 33: em\_htg\_mus:\*
   
 34: em\_htg\_pln:\*
   
 35: em\_htg\_rod:\*
   
 36: em\_htg\_mam:\*
   
 37: em\_htg\_vrt:\*
   
 38: em\_sy:\*
   
 39: em\_htgo\_hum:\*
   
 40: em\_htgo\_mus:\*
   
 41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query Score	Match	Length	DB	ID	Description
1	1344	100.0	2230	10	BC006636	BC006636 Mus muscu
2	1344	100.0	2478	10	AF112151	AF112151 Mus muscu
3	1233.6	91.8	2499	10	AF112153	AF112153 Rattus no
4	1232	91.7	2304	10	AF137350	AF137350 Rattus no
5	1113.6	82.9	1720	6	A84086	A84086 Sequence 1
6	1113.6	82.9	2019	9	HSA133490	AJ133490 Homo sapi
7	1113.6	82.9	2126	6	BD127534	BD127534 Primer fo
8	1113.6	82.9	2126	9	AK075147	AK075147 Homo sapi
9	1113.6	82.9	2328	9	AF112152	AF112152 Homo sapi
10	1113.6	82.9	2367	9	BC022280	BC022280 Homo sapi
11	1113.6	82.9	2550	6	AR036548	AR036548 Sequence
12	1113.6	82.9	2550	6	AR173204	AR173204 Sequence
13	1113.6	82.9	2550	6	BD132822	BD132822 human ext
14	1112	82.7	2609	6	AX376340	AX376340 Sequence
15	1112	82.7	2609	6	AX403659	AX403659 Sequence
16	1097.6	81.7	2019	9	AF093118	AF093118 Homo sapi
17	604.6	45.0	853	6	BD124625	BD124625 Primer fo
18	604.6	45.0	853	6	BD126198	BD126198 Primer fo
19	604.6	45.0	1538	6	BD127158	BD127158 Primer fo
20	604.6	45.0	1538	9	AK074540	AK074540 Homo sapi
21	350.8	26.1	1440	9	HSA132819	AJ132819 Homo sapi
22	350.8	26.1	1536	9	AB030655	AB030655 Homo sapi
23	350.4	26.1	1707	6	BD155763	BD155763 Primer fo
24	350.4	26.1	1707	9	AK000980	AK000980 Homo sapi
25	349.2	26.0	1480	6	AX023967	AX023967 Sequence
26	349.2	26.0	1561	9	BC010456	BC010456 Homo sapi
27	349.2	26.0	1866	9	AK075453	AK075453 Homo sapi
28	347.6	25.9	1757	6	AX577988	AX577988 Sequence
29	347.6	25.9	1757	9	AF109121	AF109121 Homo sapi
30	347.6	25.9	1875	6	AX201326	AX201326 Sequence
31	347.6	25.9	1875	6	AX464184	AX464184 Sequence
32	347.6	25.9	2018	6	AR095382	AR095382 Sequence
33	344.4	25.6	1778	10	AF046870	AF046870 Cricetulu

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OM nucleic - nucleic search, using sw model

Run on: December 12, 2003, 21:43:31 ; Search time 343.399 Seconds  
(without alignments)  
10565.088 Million cell updates/sec

Title: US-09-674-330A-1  
Perfect score: 1344  
Sequence: 1 atgccaggattaaaaaggat.....atgtgtcgcatatccgttc 1344

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_19Jun03:  
1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:  
2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:  
3: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:  
4: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:  
5: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:  
6: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:  
7: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:  
8: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:  
9: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:  
10: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:  
11: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:  
12: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:  
13: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:  
14: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:  
15: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:  
16: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:  
17: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:  
18: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:  
19: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:  
20: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:  
21: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:  
22: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:  
23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:  
24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:  
25: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	1344	100.0	1344	21	AAZ39383	Smooth muscle prol
2	1344	100.0	2233	21	AAZ39384	Smooth muscle prol
3	1344	100.0	2233	21	AAZ40029	Full length mouse
4	1327.4	98.8	1383	21	AAZ39386	Smooth muscle prol
5	1327.4	98.8	2429	21	AAZ39387	Smooth muscle prol
6	1327.4	98.8	2429	21	AAZ40031	Full length mouse
7	1269	94.4	1269	21	AAZ39385	Smooth muscle prol
8	1269	94.4	1269	21	AAZ39388	Smooth muscle prol
9	1113.6	82.9	1347	24	ABL52528	Human UP50 cDNA se
10	1113.6	82.9	1720	19	AAV62432	Human EEGF genomic
11	1113.6	82.9	1720	24	ABK13627	Human cDNA encodin
12	1113.6	82.9	2126	22	AAK94505	Human full-length
13	1113.6	82.9	2328	21	AAZ40027	Full length human
14	1113.6	82.9	2362	20	AAX07567	Homo sapiens fetal
15	1113.6	82.9	2362	21	AAZ39892	cDNA sequence of t
16	1113.6	82.9	2550	20	AAX05359	Human extracellula
17	1112	82.7	2509	20	AAX37670	Human EGF-like hom
18	1112	82.7	2609	22	AAS46128	Human DNA encoding
19	1112	82.7	2609	22	AAC86968	Nucleotide sequenc
20	1112	82.7	2609	25	ACA57886	Human PRO210 cDNA.
21	1112	82.7	2609	25	ACA60458	Novel human secret
22	1112	82.7	2609	25	ABX98356	Human cDNA encodin
23	1112	82.7	2609	25	ABX98858	Novel human secret
24	1112	82.7	2609	25	ACA04448	Novel human secret
25	1112	82.7	2609	25	ACA04928	Novel human secret
26	1112	82.7	2609	25	ACA05903	Human secreted/tra
27	1112	82.7	2609	25	ABX97947	Human PRO polynucl
28	1112	82.7	2609	25	ABX78731	Human PRO polynucl
29	1112	82.7	2609	25	ABX75744	Human cDNA encodin
30	1112	82.7	2609	25	ABX76949	Human PRO polynucl
31	1112	82.7	2609	25	ABX16789	Human cDNA encodin
32	1097.6	81.7	2019	24	ABT10172	Human breast cance
33	1000.8	74.5	1228	18	AAT89380	Human extracellula
34	922.2	68.6	1254	21	AAZ61672	cDNA encoding rat
35	922.2	68.6	1254	22	AAC99605	Skin cell cDNA, SE
36	920.2	68.5	1260	24	ABL34757	Rat cDNA isolated
37	650	48.4	778	20	AAX37673	Human PRO protein
38	604.6	45.0	853	22	AAK91596	Human cDNA 5'-end
39	604.6	45.0	853	22	AAK93169	Human cDNA clone r
40	604.6	45.0	1538	22	AAK94129	Human full-length
41	516	38.4	680	21	AAA44245	Human secreted exp
42	350.4	26.1	1707	22	AAH13771	Human cDNA sequenc
43	349.2	26.0	1480	21	AAA14608	cDNA encoding a hu
44	349.2	26.0	1525	18	AAT88974	Human extracellula
45	349.2	26.0	1531	20	AAX60351	Extracellular prot

#### ALIGNMENTS

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OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 12:56:44 ; Search time 90.1381 Seconds  
(without alignments)  
6581.220 Million cell updates/sec

Title: US-09-674-330A-1  
Perfect score: 1344  
Sequence: 1 atgccaggattaaaaaggat.....atgtgtcgcgatccgttc 1344

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:  
1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*

2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*

3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*

4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*

5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\*

6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Query				Description	
No.	Score	Match	Length	DB	ID	Description
1	1113.6	82.9	2550	2	US-08-884-072-2	Sequence 2, Appli
2	1113.6	82.9	2550	4	US-09-212-168-2	Sequence 2, Appli
3	922.2	68.6	1254	4	US-09-312-283C-67	Sequence 67, Appli
4	920.2	68.5	1260	3	US-09-188-930-67	Sequence 67, Appli
5	349.2	26.0	1531	2	US-08-833-963C-1	Sequence 1, Appli
6	347.6	25.9	2018	3	US-08-980-514-2	Sequence 2, Appli
7	289.4	21.5	1018	3	US-09-188-930-259	Sequence 259, App
8	289.4	21.5	1018	4	US-09-312-283C-259	Sequence 259, App
9	244.6	18.2	2512	4	US-09-248-757-1	Sequence 1, Appli
10	102.8	7.6	3373	2	US-08-897-443-2	Sequence 2, Appli
11	92.4	6.9	401	4	US-09-643-597-278	Sequence 278, App

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OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 18:05:35 ; Search time 424.12 Seconds  
(without alignments)  
10532.199 Million cell updates/sec

Title: US-09-674-330A-1

Perfect score: 1344

Sequence: 1.atgccaggattaaaaaggat.....atgtgtcgcatatccgttc 1344

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2201672 seqs, 1661799599 residues

Total number of hits satisfying chosen parameters: 4403344

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published\_Applications\_NA:\*

1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*

2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*

3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*

4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*

5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*

6: /cgn2\_6/ptodata/1/pubpna/PECTUS\_PUBCOMB.seq:\*

7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*

8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*

9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*

10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*

11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*

12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*

13: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq2:\*

14: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*

15: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*

16: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*

17: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*

18: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query					Description
	Score	Match	Length	DB	ID	
1	1233.6	91.8	2499	15	US-10-175-523-164	Sequence 164, App
2	1113.6	82.9	1717	9	US-09-275-805-1	Sequence 1, Appli
3	1113.6	82.9	2362	9	US-09-083-002-1	Sequence 1, Appli
4	1113.6	82.9	2362	14	US-10-041-016-1	Sequence 1, Appli
5	1113.6	82.9	2550	9	US-09-836-561-2	Sequence 2, Appli
6	1112	82.7	2609	13	US-10-199-672-407	Sequence 407, App
7	1112	82.7	2609	13	US-10-187-749-407	Sequence 407, App
8	1112	82.7	2609	13	US-10-194-457-407	Sequence 407, App
9	1112	82.7	2609	13	US-10-184-642-407	Sequence 407, App
10	1112	82.7	2609	13	US-10-196-747-407	Sequence 407, App
11	1112	82.7	2609	13	US-10-173-689-407	Sequence 407, App
12	1112	82.7	2609	13	US-10-173-690-407	Sequence 407, App
13	1112	82.7	2609	13	US-10-173-691-407	Sequence 407, App
14	1112	82.7	2609	13	US-10-173-692-407	Sequence 407, App
15	1112	82.7	2609	13	US-10-173-694-407	Sequence 407, App
16	1112	82.7	2609	13	US-10-173-698-407	Sequence 407, App
17	1112	82.7	2609	13	US-10-173-699-407	Sequence 407, App
18	1112	82.7	2609	13	US-10-173-707-407	Sequence 407, App
19	1112	82.7	2609	13	US-10-174-569-407	Sequence 407, App
20	1112	82.7	2609	13	US-10-174-583-407	Sequence 407, App
21	1112	82.7	2609	13	US-10-174-587-407	Sequence 407, App
22	1112	82.7	2609	13	US-10-174-589-407	Sequence 407, App
23	1112	82.7	2609	13	US-10-174-591-407	Sequence 407, App
24	1112	82.7	2609	13	US-10-175-736-407	Sequence 407, App
25	1112	82.7	2609	13	US-10-175-742-407	Sequence 407, App
26	1112	82.7	2609	13	US-10-175-744-407	Sequence 407, App
27	1112	82.7	2609	13	US-10-175-745-407	Sequence 407, App
28	1112	82.7	2609	13	US-10-175-748-407	Sequence 407, App
29	1112	82.7	2609	13	US-10-175-751-407	Sequence 407, App
30	1112	82.7	2609	13	US-10-175-754-407	Sequence 407, App
31	1112	82.7	2609	13	US-10-176-480-407	Sequence 407, App
32	1112	82.7	2609	13	US-10-176-489-407	Sequence 407, App
33	1112	82.7	2609	13	US-10-176-754-407	Sequence 407, App
34	1112	82.7	2609	13	US-10-176-755-407	Sequence 407, App
35	1112	82.7	2609	13	US-10-176-759-407	Sequence 407, App
36	1112	82.7	2609	13	US-10-176-920-407	Sequence 407, App
37	1112	82.7	2609	13	US-10-176-922-407	Sequence 407, App
38	1112	82.7	2609	13	US-10-176-924-407	Sequence 407, App
39	1112	82.7	2609	13	US-10-176-984-407	Sequence 407, App
40	1112	82.7	2609	13	US-10-179-508-407	Sequence 407, App
41	1112	82.7	2609	13	US-10-179-512-407	Sequence 407, App
42	1112	82.7	2609	13	US-10-179-515-407	Sequence 407, App
43	1112	82.7	2609	13	US-10-066-198-14	Sequence 14, Appl
44	1112	82.7	2609	13	US-10-173-702-407	Sequence 407, App
45	1112	82.7	2609	13	US-10-173-703-407	Sequence 407, App

## ALIGNMENTS

RESULT 1  
US-10-175-523-164

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OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 12:45:39 ; Search time 2631.5 Seconds  
(without alignments)  
12413.176 Million cell updates/sec

Title: US-09-674-330A-1

Perfect score: 1344

Sequence: 1 atgccaggattaaaaaggat.....atgtgtcgcatatccgttc 1344

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:  
1: em\_estba:  
2: em\_esthum:  
3: em\_estin:  
4: em\_estmu:  
5: em\_estov:  
6: em\_estpl:  
7: em\_estro:  
8: em\_htc:  
9: gb\_est1:  
10: gb\_est2:  
11: gb\_htc:  
12: gb\_est3:  
13: gb\_est4:  
14: gb\_est5:  
15: em\_estfun:  
16: em\_estom:  
17: em\_gss\_hum:  
18: em\_gss\_inv:  
19: em\_gss\_pln:  
20: em\_gss\_vrt:  
21: em\_gss\_fun:  
22: em\_gss\_mam:  
23: em\_gss\_mus:  
24: em\_gss\_pro:  
25: em\_gss\_rod:  
26: em\_gss\_phg:  
27: em\_gss\_vrl:

28: gb\_gss1:  
29: gb\_gss2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	1344	100.0	1835	11	AK085170	AK085170 Mus muscu
2	1344	100.0	5831	11	AK090129	AK090129 Mus muscu
3	1017.2	75.7	2423	11	CNSLT1I9S	BX248290 human ful
4	771	57.4	980	13	BU520272	BU520272 AGENCOURT
5	761.8	56.7	870	13	BQ930927	BQ930927 AGENCOURT
6	760.8	56.6	796	12	BI453348	BI453348 603173067
7	741.2	55.1	1796	11	AK084895	AK084895 Mus muscu
8	731	54.4	1201	13	BX439363	BX439363 BX439363
9	708	52.7	717	12	BI251219	BI251219 602994427
10	706.4	52.6	1014	12	BM921371	BM921371 AGENCOURT
11	706	52.5	912	13	BU149085	BU149085 AGENCOURT
12	682.8	50.8	815	10	BG174360	BG174360 602336371
13	679	50.5	877	13	BX326257	BX326257 BX326257
14	678.2	50.5	842	13	BX367825	BX367825 BX367825
15	672.8	50.1	996	13	BQ720516	BQ720516 AGENCOURT
16	660.8	49.2	888	13	BX346924	BX346924 BX346924
17	655.8	48.8	841	14	CD172152	CD172152 AGENCOURT
18	649.4	48.3	954	12	BM545444	BM545444 AGENCOURT
19	643.4	47.9	904	13	BQ716569	BQ716569 AGENCOURT
20	642.6	47.8	952	13	BU148724	BU148724 AGENCOURT
21	641.6	47.7	930	13	BX349066	BX349066 BX349066
22	636.6	47.4	854	13	BX347366	BX347366 BX347366
c 23	634.8	47.2	870	13	BX429526	BX429526 BX429526
24	600	44.6	762	14	CB595725	CB595725 AGENCOURT
c 25	580.4	43.2	923	13	BX326104	BX326104 BX326104
c 26	580.2	43.2	954	13	BX371974	BX371974 BX371974
27	562.4	41.8	654	14	CB595181	CB595181 AGENCOURT
c 28	557.4	41.5	906	13	BX388741	BX388741 BX388741
29	557.2	41.5	914	13	BX450129	BX450129 BX450129
30	556	41.4	822	10	BG109391	BG109391 602280448
31	550.6	41.0	891	10	BF339448	BF339448 602039102
32	538.8	40.1	867	13	BX326018	BX326018 BX326018
33	535	39.8	778	13	BU750981	BU750981 CH3#037_B
34	531.2	39.5	894	13	BX408562	BX408562 BX408562
35	530.4	39.5	644	12	BG938621	BG938621 cn27c11.x
36	518	38.5	882	12	BI825121	BI825121 603038662
37	502.6	37.4	835	13	BQ718885	BQ718885 AGENCOURT
38	498.8	37.1	1101	10	BG245848	BG245848 602358649
39	497	37.0	880	12	BI764020	BI764020 603043221
40	489.4	36.4	680	9	AW106432	AW106432 um27g01.y
41	486.2	36.2	636	14	BY753400	BY753400 BY753400
42	482.2	35.9	627	12	BI183862	BI183862 UNL-P-FN-
c 43	481.4	35.8	627	10	BF090699	BF090699 QV2-NT004
44	472.4	35.1	933	13	BQ716088	BQ716088 AGENCOURT
45	470	35.0	912	12	BI768516	BI768516 603057118

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OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 07:36:19 ; Search time 4997.97 Seconds  
(without alignments)  
11320.190 Million cell updates/sec

Title: US-09-674-330A-6

Perfect score: 1383

Sequence: 1 atgggacctaagaagttcga.....atgtgtcgcatatccgttc 1383

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:  
1: gb\_ba:  
2: gb\_htg:  
3: gb\_in:  
4: gb\_om:  
5: gb\_ov:  
6: gb\_pat:  
7: gb\_ph:  
8: gb\_pl:  
9: gb\_pr:  
10: gb\_ro:  
11: gb\_sts:  
12: gb\_sy:  
13: gb\_un:  
14: gb\_vi:  
15: em\_ba:  
16: em\_fun:  
17: em\_hum:  
18: em\_in:  
19: em\_mu:  
20: em\_om:  
21: em\_or:  
22: em\_ov:  
23: em\_pat:  
24: em\_ph:  
25: em\_pl:  
26: em\_ro:  
27: em\_sts:

```

28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1327.4	96.0	2230	10	BC006636	BC006636 Mus muscu
2	1327.4	96.0	2478	10	AF112151	AF112151 Mus muscu
3	1217	88.0	2499	10	AF112153	AF112153 Rattus no
4	1215.4	87.9	2304	10	AF137350	AF137350 Rattus no
5	1098.6	79.4	1720	6	A84086	A84086 Sequence 1
6	1098.6	79.4	2019	9	HSA133490	AJ133490 Homo sapi
7	1098.6	79.4	2126	6	BD127534	BD127534 Primer fo
8	1098.6	79.4	2126	9	AK075147	AK075147 Homo sapi
9	1098.6	79.4	2328	9	AF112152	AF112152 Homo sapi
10	1098.6	79.4	2367	9	BC022280	BC022280 Homo sapi
11	1098.6	79.4	2550	6	AR036548	AR036548 Sequence
12	1098.6	79.4	2550	6	AR173204	AR173204 Sequence
13	1098.6	79.4	2550	6	BD132822	BD132822 human ext
14	1097	79.3	2609	6	AX376340	AX376340 Sequence
15	1097	79.3	2609	6	AX403659	AX403659 Sequence
16	1082.6	78.3	2019	9	AF093118	AF093118 Homo sapi
17	604.6	43.7	853	6	BD124625	BD124625 Primer fo
18	604.6	43.7	853	6	BD126198	BD126198 Primer fo
19	604.6	43.7	1538	6	BD127158	BD127158 Primer fo
20	604.6	43.7	1538	9	AK074540	AK074540 Homo säpi
21	350.8	25.4	1440	9	HSA132819	AJ132819 Homo sapi
22	350.8	25.4	1536	9	AB030655	AB030655 Homo sapi
23	350.4	25.3	1707	6	BD155763	BD155763 Primer fo
24	350.4	25.3	1707	9	AK000980	AK000980 Homo sapi
25	349.2	25.2	1480	6	AX023967	AX023967 Sequence
26	349.2	25.2	1561	9	BC010456	BC010456 Homo sapi
27	349.2	25.2	1866	9	AK075453	AK075453 Homo sapi
28	347.6	25.1	1757	6	AX577988	AX577988 Sequence
29	347.6	25.1	1757	9	AF109121	AF109121 Homo sapi
30	347.6	25.1	1875	6	AX201326	AX201326 Sequence
31	347.6	25.1	1875	6	AX464184	AX464184 Sequence
32	347.6	25.1	2018	6	AR095382	AR095382 Sequence
33	344.4	24.9	1778	10	AF046870	AF046870 Cricetulu

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OM nucleic - nucleic search, using sw model

Run on: December 12, 2003, 21:43:31 ; Search time 353.364 Seconds  
(without alignments)  
10565.088 Million cell updates/sec

Title: US-09-674-330A-6  
Perfect score: 1383  
Sequence: 1 atgggacctagaagttcga.....atgtgtcgccagtatccgttc 1383

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_19Jun03:  
1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:\*

2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:\*

3: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:\*

4: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:\*

5: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:\*

6: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:\*

7: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:\*

8: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:\*

9: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:\*

10: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:\*

11: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:\*

12: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:\*

13: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:\*

14: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:\*

15: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:\*

16: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:\*

17: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:\*

18: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:\*

19: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:\*

20: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:\*

21: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:\*

22: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:\*

23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:\*

24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:\*

25: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query					Description
	Score	Match	Length	DB	ID	
1	1383	100.0	1383	21	AAZ39386	Smooth muscle prol
2	1383	100.0	2429	21	AAZ39387	Smooth muscle prol
3	1383	100.0	2429	21	AAZ40031	Full length mouse
4	1327.4	96.0	1344	21	AAZ39383	Smooth muscle prol
5	1327.4	96.0	2233	21	AAZ39384	Smooth muscle prol
6	1327.4	96.0	2233	21	AAZ40029	Full length mouse
7	1269	91.8	1269	21	AAZ39385	Smooth muscle prol
8	1269	91.8	1269	21	AAZ39388	Smooth muscle prol
9	1098.6	79.4	1347	24	ABL52528	Human UP50 cDNA se
10	1098.6	79.4	1720	19	AAV62432	Human EEGF genomic
11	1098.6	79.4	1720	24	ABK13627	Human cDNA encodin
12	1098.6	79.4	2126	22	AAK94505	Human full-length
13	1098.6	79.4	2328	21	AAZ40027	Full length human
14	1098.6	79.4	2362	20	AAX07567	Homo sapiens fetal
15	1098.6	79.4	2362	21	AAZ39892	cDNA sequence of t
16	1098.6	79.4	2550	20	AAX05359	Human extracellula
17	1097	79.3	2509	20	AAX37670	Human EGF-like hom
18	1097	79.3	2609	22	AAS46128	Human DNA encoding
19	1097	79.3	2609	22	AAC86968	Nucleotide sequenc
20	1097	79.3	2609	25	ACA57886	Human PRO210 cDNA.
21	1097	79.3	2609	25	ACA60458	Novel human secret
22	1097	79.3	2609	25	ABX98356	Human cDNA encodin
23	1097	79.3	2609	25	ABX98858	Novel human secret
24	1097	79.3	2609	25	ACA04448	Novel human secret
25	1097	79.3	2609	25	ACA04928	Novel human secret
26	1097	79.3	2609	25	ACA05903	Human secreted/tra
27	1097	79.3	2609	25	ABX97947	Human PRO polynucl
28	1097	79.3	2609	25	ABX78731	Human PRO polynucl
29	1097	79.3	2609	25	ABX75744	Human cDNA encodin
30	1097	79.3	2609	25	ABX76949	Human PRO polynucl
31	1097	79.3	2609	25	ABX16789	Human cDNA encodin
32	1082.6	78.3	2019	24	ABT10172	Human breast cance
33	1000.8	72.4	1228	18	AAT89380	Human extracellula
34	922.2	66.7	1254	21	AAZ61672	cDNA encoding rat
35	922.2	66.7	1254	22	AAC99605	Skin cell cDNA, SE
36	920.2	66.5	1260	24	ABL34757	Rat cDNA isolated
37	650	47.0	778	20	AAX37673	Human PRO protein
38	604.6	43.7	853	22	AAK91596	Human cDNA 5'-end
39	604.6	43.7	853	22	AAK93169	Human cDNA clone r
40	604.6	43.7	1538	22	AAK94129	Human full-length
41	527.6	38.1	680	21	AAA44245	Human secreted exp
42	350.4	25.3	1707	22	AAH13771	Human cDNA sequenc
43	349.2	25.2	1480	21	AAA14608	cDNA encoding a hu
44	349.2	25.2	1525	18	AAT88974	Human extracellula
45	349.2	25.2	1531	20	AAX60351	Extracellular prot

#### ALIGNMENTS

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OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 12:56:44 ; Search time 92.7538 Seconds  
(without alignments)  
6581.220 Million cell updates/sec

Title: US-09-674-330A-6

Perfect score: 1383

Sequence: 1 atgggacctaagaagtttcga.....atgtgtcgccagtatccgttc 1383

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:  
1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB	
1	1098.6	79.4	2550	2	US-08-884-072-2	Sequence 2, Appli
2	1098.6	79.4	2550	4	US-09-212-168-2	Sequence 2, Appli
3	922.2	66.7	1254	4	US-09-312-283C-67	Sequence 67, Appli
4	920.2	66.5	1260	3	US-09-188-930-67	Sequence 67, Appli
5	349.2	25.2	1531	2	US-08-833-963C-1	Sequence 1, Appli
6	347.6	25.1	2018	3	US-08-980-514-2	Sequence 2, Appli
7	289.4	20.9	1018	3	US-09-188-930-259	Sequence 259, App
8	289.4	20.9	1018	4	US-09-312-283C-259	Sequence 259, App
9	244.6	17.7	2512	4	US-09-248-757-1	Sequence 1, Appli
10	102.8	7.4	3373	2	US-08-897-443-2	Sequence 2, Appli
11	92.4	6.7	401	4	US-09-643-597-278	Sequence 278, App

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 18:05:35 ; Search time 436.427 Seconds  
(without alignments)  
10532.199 Million cell updates/sec

Title: US-09-674-330A-6  
Perfect score: 1383  
Sequence: 1 atgggacctaagaagttcga.....atgtgtcgccagtatccgttc 1383

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2201672 seqs, 1661799599 residues

Total number of hits satisfying chosen parameters: 4403344

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_NA:  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*

2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*

3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*

4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*

5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*

6: /cgn2\_6/ptodata/1/pubpna/PCJTUS\_PUBCOMB.seq:\*

7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*

8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*

9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*

10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*

11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*

12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*

13: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq2:\*

14: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*

15: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*

16: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*

17: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*

18: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	1217	88.0	2499	15	US-10-175-523-164	Sequence 164, App
2	1098.6	79.4	1717	9	US-09-275-805-1	Sequence 1, Appli
3	1098.6	79.4	2362	9	US-09-083-002-1	Sequence 1, Appli
4	1098.6	79.4	2362	14	US-10-041-016-1	Sequence 1, Appli
5	1098.6	79.4	2550	9	US-09-836-561-2	Sequence 2, Appli
6	1097	79.3	2609	13	US-10-199-672-407	Sequence 407, App
7	1097	79.3	2609	13	US-10-187-749-407	Sequence 407, App
8	1097	79.3	2609	13	US-10-194-457-407	Sequence 407, App
9	1097	79.3	2609	13	US-10-184-642-407	Sequence 407, App
10	1097	79.3	2609	13	US-10-196-747-407	Sequence 407, App
11	1097	79.3	2609	13	US-10-173-689-407	Sequence 407, App
12	1097	79.3	2609	13	US-10-173-690-407	Sequence 407, App
13	1097	79.3	2609	13	US-10-173-691-407	Sequence 407, App
14	1097	79.3	2609	13	US-10-173-692-407	Sequence 407, App
15	1097	79.3	2609	13	US-10-173-694-407	Sequence 407, App
16	1097	79.3	2609	13	US-10-173-698-407	Sequence 407, App
17	1097	79.3	2609	13	US-10-173-699-407	Sequence 407, App
18	1097	79.3	2609	13	US-10-173-707-407	Sequence 407, App
19	1097	79.3	2609	13	US-10-174-569-407	Sequence 407, App
20	1097	79.3	2609	13	US-10-174-583-407	Sequence 407, App
21	1097	79.3	2609	13	US-10-174-587-407	Sequence 407, App
22	1097	79.3	2609	13	US-10-174-589-407	Sequence 407, App
23	1097	79.3	2609	13	US-10-174-591-407	Sequence 407, App
24	1097	79.3	2609	13	US-10-175-736-407	Sequence 407, App
25	1097	79.3	2609	13	US-10-175-742-407	Sequence 407, App
26	1097	79.3	2609	13	US-10-175-744-407	Sequence 407, App
27	1097	79.3	2609	13	US-10-175-745-407	Sequence 407, App
28	1097	79.3	2609	13	US-10-175-748-407	Sequence 407, App
29	1097	79.3	2609	13	US-10-175-751-407	Sequence 407, App
30	1097	79.3	2609	13	US-10-175-754-407	Sequence 407, App
31	1097	79.3	2609	13	US-10-176-480-407	Sequence 407, App
32	1097	79.3	2609	13	US-10-176-489-407	Sequence 407, App
33	1097	79.3	2609	13	US-10-176-754-407	Sequence 407, App
34	1097	79.3	2609	13	US-10-176-755-407	Sequence 407, App
35	1097	79.3	2609	13	US-10-176-759-407	Sequence 407, App
36	1097	79.3	2609	13	US-10-176-920-407	Sequence 407, App
37	1097	79.3	2609	13	US-10-176-922-407	Sequence 407, App
38	1097	79.3	2609	13	US-10-176-924-407	Sequence 407, App
39	1097	79.3	2609	13	US-10-176-984-407	Sequence 407, App
40	1097	79.3	2609	13	US-10-179-508-407	Sequence 407, App
41	1097	79.3	2609	13	US-10-179-512-407	Sequence 407, App
42	1097	79.3	2609	13	US-10-179-515-407	Sequence 407, App
43	1097	79.3	2609	13	US-10-066-198-14	Sequence 14, Appl
44	1097	79.3	2609	13	US-10-173-702-407	Sequence 407, App
45	1097	79.3	2609	13	US-10-173-703-407	Sequence 407, App

## ALIGNMENTS

RESULT 1  
US-10-175-523-164

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OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 12:45:39 ; Search time 2707.86 Seconds  
(without alignments)  
12413.176 Million cell updates/sec

Title: US-09-674-330A-6

Perfect score: 1383

Sequence: 1 atgggacctagaagttcga.....atgtgtcgcatatccgttc 1383

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:  
1: em\_estba:  
2: em\_esthum:  
3: em\_estin:  
4: em\_estmu:  
5: em\_estov:  
6: em\_estpl:  
7: em\_estro:  
8: em\_htc:  
9: gb\_est1:  
10: gb\_est2:  
11: gb\_htc:  
12: gb\_est3:  
13: gb\_est4:  
14: gb\_est5:  
15: em\_estfun:  
16: em\_estom:  
17: em\_gss\_hum:  
18: em\_gss\_inv:  
19: em\_gss\_pln:  
20: em\_gss\_vrt:  
21: em\_gss\_fun:  
22: em\_gss\_mam:  
23: em\_gss\_mus:  
24: em\_gss\_pro:  
25: em\_gss\_rod:  
26: em\_gss\_phg:  
27: em\_gss\_vrl:

28: gb\_gss1:  
29: gb\_gss2:  
\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query					Description
		Match	Length	DB	ID	%	
1	1327.4	96.0	1835	11	AK085170		AK085170 Mus muscu
2	1327.4	96.0	5831	11	AK090129		AK090129 Mus muscu
3	1017.2	73.6	2423	11	CNSLT1I9S		BX248290 human ful
4	760.8	55.0	796	12	BI453348		BI453348 603173067
5	754.4	54.5	980	13	BU520272		BU520272 AGENCOURT
6	745.2	53.9	870	13	BQ930927		BQ930927 AGENCOURT
7	724.6	52.4	1796	11	AK084895		AK084895 Mus muscu
8	716	51.8	1201	13	BX439363		BX439363 BX439363
9	708	51.2	717	12	BI251219		BI251219 602994427
10	691.4	50.0	1014	12	BM921371		BM921371 AGENCOURT
11	689.4	49.8	912	13	BU149085		BU149085 AGENCOURT
12	679	49.1	877	13	BX326257		BX326257 BX326257
13	678.2	49.0	842	13	BX367825		BX367825 BX367825
14	672.8	48.6	996	13	BQ720516		BQ720516 AGENCOURT
15	666.2	48.2	815	10	BG174360		BG174360 602336371
16	660.8	47.8	888	13	BX346924		BX346924 BX346924
17	655.8	47.4	841	14	CD172152		CD172152 AGENCOURT
18	649.4	47.0	954	12	BM545444		BM545444 AGENCOURT
19	643.4	46.5	904	13	BQ716569		BQ716569 AGENCOURT
20	642.6	46.5	952	13	BU148724		BU148724 AGENCOURT
21	641.6	46.4	930	13	BX349066		BX349066 BX349066
22	636.6	46.0	854	13	BX347366		BX347366 BX347366
c 23	634.8	45.9	870	13	BX429526		BX429526 BX429526
24	600	43.4	762	14	CB595725		CB595725 AGENCOURT
c 25	580.4	42.0	923	13	BX326104		BX326104 BX326104
c 26	580.2	42.0	954	13	BX371974		BX371974 BX371974
27	562.4	40.7	654	14	CB595181		CB595181 AGENCOURT
c 28	557.4	40.3	906	13	BX388741		BX388741 BX388741
29	557.2	40.3	914	13	BX450129		BX450129 BX450129
30	556	40.2	822	10	BG109391		BG109391 602280448
31	554.4	40.1	1101	10	BG245848		BG245848 602358649
32	550.6	39.8	891	10	BF339448		BF339448 602039102
33	538.8	39.0	867	13	BX326018		BX326018 BX326018
34	535	38.7	778	13	BU750981		BU750981 CH3#037_B
35	531.2	38.4	894	13	BX408562		BX408562 BX408562
36	530.4	38.4	644	12	BG938621		BG938621 cn27c11.x
37	503	36.4	882	12	BI825121		BI825121 603038662
38	487.6	35.3	835	13	BQ718885		BQ718885 AGENCOURT
39	482.2	34.9	627	12	BI183862		BI183862 UNL-P-FN-
40	482	34.9	880	12	BI764020		BI764020 603043221
c 41	481.4	34.8	627	10	BF090699		BF090699 QV2-NT004
42	472.8	34.2	680	9	AW106432		AW106432 um27g01.y
43	472.4	34.2	933	13	BQ716088		BQ716088 AGENCOURT
44	470	34.0	912	12	BI768516		BI768516 603057118
45	469.6	34.0	636	14	BY753400		BY753400 BY753400

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OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 07:36:19 ; Search time 4585.99 Seconds  
(without alignments)  
11320.190 Million cell updates/sec

Title: US-09-674-330A-10

Perfect score: 1269

Sequence: 1 cagtgcacaaacggctttga.....atgtgtcgcatatccgttc 1269

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:  
1: gb\_ba:  
2: gb\_htg:  
3: gb\_in:  
4: gb\_om:  
5: gb\_ov:  
6: gb\_pat:  
7: gb\_ph:  
8: gb\_pl:  
9: gb\_pr:  
10: gb\_ro:  
11: gb\_sts:  
12: gb\_sy:  
13: gb\_un:  
14: gb\_vi:  
15: em\_ba:  
16: em\_fun:  
17: em\_hum:  
18: em\_in:  
19: em\_mu:  
20: em\_om:  
21: em\_or:  
22: em\_ov:  
23: em\_pat:  
24: em\_ph:  
25: em\_pl:  
26: em\_ro:  
27: em\_sts:

```

28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1269	100.0	2230	10	BC006636	BC006636 Mus muscu
2	1269	100.0	2478	10	AF112151	AF112151 Mus muscu
3	1165	91.8	2499	10	AF112153	AF112153 Rattus no
4	1163.4	91.7	2304	10	AF137350	AF137350 Rattus no
5	1056.2	83.2	1720	6	A84086	A84086 Sequence 1
6	1056.2	83.2	2019	9	HSA133490	AJ133490 Homo sapi
7	1056.2	83.2	2126	6	BD127534	BD127534 Primer fo
8	1056.2	83.2	2126	9	AK075147	AK075147 Homo sapi
9	1056.2	83.2	2328	9	AF112152	AF112152 Homo sapi
10	1056.2	83.2	2367	9	BC022280	BC022280 Homo sapi
11	1056.2	83.2	2550	6	AR036548	AR036548 Sequence
12	1056.2	83.2	2550	6	AR173204	AR173204 Sequence
13	1056.2	83.2	2550	6	BD132822	BD132822 human ext
14	1054.6	83.1	2609	6	AX376340	AX376340 Sequence
15	1054.6	83.1	2609	6	AX403659	AX403659 Sequence
16	1040.2	82.0	2019	9	AF093118	AF093118 Homo sapi
17	604.6	47.6	853	6	BD124625	BD124625 Primer fo
18	604.6	47.6	853	6	BD126198	BD126198 Primer fo
19	604.6	47.6	1538	6	BD127158	BD127158 Primer fo
20	604.6	47.6	1538	9	AK074540	AK074540 Homo sapi
21	350.4	27.6	1440	9	HSA132819	AJ132819 Homo sapi
22	350.4	27.6	1536	9	AB030655	AB030655 Homo sapi
23	350	27.6	1707	6	BD155763	BD155763 Primer fo
24	350	27.6	1707	9	AK000980	AK000980 Homo sapi
25	348.8	27.5	1480	6	AX023967	AX023967 Sequence
26	348.8	27.5	1561	9	BC010456	BC010456 Homo sapi
27	348.8	27.5	1866	9	AK075453	AK075453 Homo sapi
28	347.2	27.4	1757	6	AX577988	AX577988 Sequence
29	347.2	27.4	1757	9	AF109121	AF109121 Homo sapi
30	347.2	27.4	1875	6	AX201326	AX201326 Sequence
31	347.2	27.4	1875	6	AX464184	AX464184 Sequence
32	347.2	27.4	2018	6	AR095382	AR095382 Sequence
33	344	27.1	1350	6	AX577913	AX577913 Sequence

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OM nucleic - nucleic search, using sw model

Run on: December 12, 2003, 21:43:31 ; Search time 324.236 Seconds  
(without alignments)  
10565.088 Million cell updates/sec

Title: US-09-674-330A-10  
Perfect score: 1269  
Sequence: 1 cagtgcacaaacggcttga.....atgtgtcgcatatccgttc 1269

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_19Jun03:  
1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:\*2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:\*3: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:\*4: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:\*5: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:\*6: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:\*7: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:\*8: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:\*9: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:\*10: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:\*11: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:\*12: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:\*13: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:\*14: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:\*15: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:\*16: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:\*17: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:\*18: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:\*19: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:\*20: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:\*21: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:\*22: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:\*23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:\*24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:\*25: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	1269	100.0	1269	21	AAZ39385	Smooth muscle prol
2	1269	100.0	1269	21	AAZ39388	Smooth muscle prol
3	1269	100.0	1344	21	AAZ39383	Smooth muscle prol
4	1269	100.0	1383	21	AAZ39386	Smooth muscle prol
5	1269	100.0	2233	21	AAZ39384	Smooth muscle prol
6	1269	100.0	2233	21	AAZ40029	Full length mouse
7	1269	100.0	2429	21	AAZ39387	Smooth muscle prol
8	1269	100.0	2429	21	AAZ40031	Full length mouse
9	1056.2	83.2	1347	24	ABL52528	Human UP50 cDNA se
10	1056.2	83.2	1720	19	AAV62432	Human EGF genomic
11	1056.2	83.2	1720	24	ABK13627	Human cDNA encodin
12	1056.2	83.2	2126	22	AAK94505	Human full-length
13	1056.2	83.2	2328	21	AAZ40027	Full length human
14	1056.2	83.2	2362	20	AAX07567	Homo sapiens fetal
15	1056.2	83.2	2362	21	AAZ39892	cDNA sequence of t
16	1056.2	83.2	2550	20	AAX05359	Human extracellula
17	1054.6	83.1	2509	20	AAX37670	Human EGF-like hom
18	1054.6	83.1	2609	22	AAS46128	Human DNA encoding
19	1054.6	83.1	2609	22	AAC86968	Nucleotide sequenc
20	1054.6	83.1	2609	25	ACA57886	Human PRO210 cDNA.
21	1054.6	83.1	2609	25	ACA60458	Novel human secret
22	1054.6	83.1	2609	25	ABX98356	Human cDNA encodin
23	1054.6	83.1	2609	25	ABX98858	Novel human secret
24	1054.6	83.1	2609	25	ACA04448	Novel human secret
25	1054.6	83.1	2609	25	ACA04928	Novel human secret
26	1054.6	83.1	2609	25	ACA05903	Human secreted/tra
27	1054.6	83.1	2609	25	ABX97947	Human PRO polynucl
28	1054.6	83.1	2609	25	ABX78731	Human PRO polynucl
29	1054.6	83.1	2609	25	ABX75744	Human cDNA encodin
30	1054.6	83.1	2609	25	ABX76949	Human PRO polynucl
31	1054.6	83.1	2609	25	ABX16789	Human cDNA encodin
32	1040.2	82.0	2019	24	ABT10172	Human breast cance
33	1000.8	78.9	1228	18	AAT89380	Human extracellula
34	922.2	72.7	1254	21	AAZ61672	cDNA encoding rat
35	922.2	72.7	1254	22	AAC99605	Skin cell cDNA, SE
36	920.2	72.5	1260	24	ABL34757	Rat cDNA isolated
37	650	51.2	778	20	AAX37673	Human PRO protein
38	604.6	47.6	853	22	AAK91596	Human cDNA 5'-end
39	604.6	47.6	853	22	AAK93169	Human cDNA clone r
40	604.6	47.6	1538	22	AAK94129	Human full-length
41	472.8	37.3	680	21	AAA44245	Human secreted exp
42	350	27.6	1707	22	AAH13771	Human cDNA sequenc
43	348.8	27.5	1480	21	AAA14608	cDNA encoding a hu
44	348.8	27.5	1525	18	AAT88974	Human extracellula
45	348.8	27.5	1531	20	AAX60351	Extracellular prot

#### ALIGNMENTS

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OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 12:56:44 ; Search time 85.1081 Seconds  
(without alignments)  
6581.220 Million cell updates/sec

Title: US-09-674-330A-10

Perfect score: 1269

Sequence: 1 cagtgcacaaacggcttga.....atgtgtcgcatatccgttc 1269

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:  
1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:  
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:  
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:  
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:  
5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:  
\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB	
1	1056.2	83.2	2550	2	US-08-884-072-2	Sequence 2, Appli
2	1056.2	83.2	2550	4	US-09-212-168-2	Sequence 2, Appli
3	922.2	72.7	1254	4	US-09-312-283C-67	Sequence 67, Appl
4	920.2	72.5	1260	3	US-09-188-930-67	Sequence 67, Appl
5	348.8	27.5	1531	2	US-08-833-963C-1	Sequence 1, Appli
6	347.2	27.4	2018	3	US-08-980-514-2	Sequence 2, Appli
7	289.4	22.8	1018	3	US-09-188-930-259	Sequence 259, App
8	289.4	22.8	1018	4	US-09-312-283C-259	Sequence 259, App
9	244.6	19.3	2512	4	US-09-248-757-1	Sequence 1, Appli
10	102.8	8.1	3373	2	US-08-897-443-2	Sequence 2, Appli
11	92.4	7.3	401	4	US-09-643-597-278	Sequence 278, App

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OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 18:05:35 ; Search time 400.453 Seconds  
(without alignments)  
10532.199 Million cell updates/sec

Title: US-09-674-330A-10

Perfect score: 1269

Sequence: 1 cagtgcacaaacggcttga.....atgtgtcgccagtatccgttc 1269

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2201672 seqs, 1661799599 residues

Total number of hits satisfying chosen parameters: 4403344

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_NA:  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*6: /cgn2\_6/ptodata/1/pubpna/PECTUS\_PUBCOMB.seq:\*7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*13: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq2:\*14: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*15: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*16: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*17: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*18: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	1165	91.8	2499	15	US-10-175-523-164	Sequence 164, App
2	1056.2	83.2	1717	9	US-09-275-805-1	Sequence 1, Appli
3	1056.2	83.2	2362	9	US-09-083-002-1	Sequence 1, Appli
4	1056.2	83.2	2362	14	US-10-041-016-1	Sequence 1, Appli
5	1056.2	83.2	2550	9	US-09-836-561-2	Sequence 2, Appli
6	1054.6	83.1	2609	13	US-10-199-672-407	Sequence 407, App
7	1054.6	83.1	2609	13	US-10-187-749-407	Sequence 407, App
8	1054.6	83.1	2609	13	US-10-194-457-407	Sequence 407, App
9	1054.6	83.1	2609	13	US-10-184-642-407	Sequence 407, App
10	1054.6	83.1	2609	13	US-10-196-747-407	Sequence 407, App
11	1054.6	83.1	2609	13	US-10-173-689-407	Sequence 407, App
12	1054.6	83.1	2609	13	US-10-173-690-407	Sequence 407, App
13	1054.6	83.1	2609	13	US-10-173-691-407	Sequence 407, App
14	1054.6	83.1	2609	13	US-10-173-692-407	Sequence 407, App
15	1054.6	83.1	2609	13	US-10-173-694-407	Sequence 407, App
16	1054.6	83.1	2609	13	US-10-173-698-407	Sequence 407, App
17	1054.6	83.1	2609	13	US-10-173-699-407	Sequence 407, App
18	1054.6	83.1	2609	13	US-10-173-707-407	Sequence 407, App
19	1054.6	83.1	2609	13	US-10-174-569-407	Sequence 407, App
20	1054.6	83.1	2609	13	US-10-174-583-407	Sequence 407, App
21	1054.6	83.1	2609	13	US-10-174-587-407	Sequence 407, App
22	1054.6	83.1	2609	13	US-10-174-589-407	Sequence 407, App
23	1054.6	83.1	2609	13	US-10-174-591-407	Sequence 407, App
24	1054.6	83.1	2609	13	US-10-175-736-407	Sequence 407, App
25	1054.6	83.1	2609	13	US-10-175-742-407	Sequence 407, App
26	1054.6	83.1	2609	13	US-10-175-744-407	Sequence 407, App
27	1054.6	83.1	2609	13	US-10-175-745-407	Sequence 407, App
28	1054.6	83.1	2609	13	US-10-175-748-407	Sequence 407, App
29	1054.6	83.1	2609	13	US-10-175-751-407	Sequence 407, App
30	1054.6	83.1	2609	13	US-10-175-754-407	Sequence 407, App
31	1054.6	83.1	2609	13	US-10-176-480-407	Sequence 407, App
32	1054.6	83.1	2609	13	US-10-176-489-407	Sequence 407, App
33	1054.6	83.1	2609	13	US-10-176-754-407	Sequence 407, App
34	1054.6	83.1	2609	13	US-10-176-755-407	Sequence 407, App
35	1054.6	83.1	2609	13	US-10-176-759-407	Sequence 407, App
36	1054.6	83.1	2609	13	US-10-176-920-407	Sequence 407, App
37	1054.6	83.1	2609	13	US-10-176-922-407	Sequence 407, App
38	1054.6	83.1	2609	13	US-10-176-924-407	Sequence 407, App
39	1054.6	83.1	2609	13	US-10-176-984-407	Sequence 407, App
40	1054.6	83.1	2609	13	US-10-179-508-407	Sequence 407, App
41	1054.6	83.1	2609	13	US-10-179-512-407	Sequence 407, App
42	1054.6	83.1	2609	13	US-10-179-515-407	Sequence 407, App
43	1054.6	83.1	2609	13	US-10-066-198-14	Sequence 14, Appl
44	1054.6	83.1	2609	13	US-10-173-702-407	Sequence 407, App
45	1054.6	83.1	2609	13	US-10-173-703-407	Sequence 407, App

## ALIGNMENTS

RESULT 1  
US-10-175-523-164

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 12:45:39 ; Search time 2484.65 Seconds  
(without alignments)  
12413.176 Million cell updates/sec

Title: US-09-674-330A-10

Perfect score: 1269

Sequence: 1 cagtgcacaaacggcttga.....atgtgtcgcatatccgttc 1269

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:  
1: em\_estba:  
2: em\_esthum:  
3: em\_estin:  
4: em\_estmu:  
5: em\_estov:  
6: em\_estpl:  
7: em\_estro:  
8: em\_htc:  
9: gb\_est1:  
10: gb\_est2:  
11: gb\_htc:  
12: gb\_est3:  
13: gb\_est4:  
14: gb\_est5:  
15: em\_estfun:  
16: em\_estom:  
17: em\_gss\_hum:  
18: em\_gss\_inv:  
19: em\_gss\_pln:  
20: em\_gss\_vrt:  
21: em\_gss\_fun:  
22: em\_gss\_mam:  
23: em\_gss\_mus:  
24: em\_gss\_pro:  
25: em\_gss\_rod:  
26: em\_gss\_phg:  
27: em\_gss\_vrl:

28: gb\_gss1:  
29: gb\_gss2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query					Description
		Match	Length	DB	ID	%	
1	1269	100.0	1835	11	AK085170		AK085170 Mus muscu
2	1269	100.0	5831	11	AK090129		AK090129 Mus muscu
3	1017.2	80.2	2423	11	CNSLT1I9S		BX248290 human ful
4	760.8	60.0	796	12	BI453348		BI453348 603173067
5	708	55.8	717	12	BI251219		BI251219 602994427
6	696	54.8	980	13	BU520272		BU520272 AGENCOURT
7	686.8	54.1	870	13	BQ930927		BQ930927 AGENCOURT
8	679	53.5	877	13	BX326257		BX326257 BX326257
9	678.2	53.4	842	13	BX367825		BX367825 BX367825
10	673.6	53.1	1201	13	BX439363		BX439363 BX439363
11	666.2	52.5	1796	11	AK084895		AK084895 Mus muscu
12	660.8	52.1	888	13	BX346924		BX346924 BX346924
13	659.6	52.0	996	13	BQ720516		BQ720516 AGENCOURT
14	655.8	51.7	841	14	CD172152		CD172152 AGENCOURT
15	649.4	51.2	954	12	BM545444		BM545444 AGENCOURT
16	649	51.1	1014	12	BM921371		BM921371 AGENCOURT
17	643.4	50.7	904	13	BQ716569		BQ716569 AGENCOURT
18	642.6	50.6	952	13	BU148724		BU148724 AGENCOURT
19	641.6	50.6	930	13	BX349066		BX349066 BX349066
20	636.6	50.2	854	13	BX347366		BX347366 BX347366
c 21	634.8	50.0	870	13	BX429526		BX429526 BX429526
22	631	49.7	912	13	BU149085		BU149085 AGENCOURT
23	607.8	47.9	815	10	BG174360		BG174360 602336371
24	600	47.3	762	14	CB595725		CB595725 AGENCOURT
c 25	580.4	45.7	923	13	BX326104		BX326104 BX326104
c 26	580.2	45.7	954	13	BX371974		BX371974 BX371974
27	562.4	44.3	654	14	CB595181		CB595181 AGENCOURT
c 28	557.4	43.9	906	13	BX388741		BX388741 BX388741
29	557.2	43.9	914	13	BX450129		BX450129 BX450129
30	556	43.8	822	10	BG109391		BG109391 602280448
31	550.6	43.4	891	10	BF339448		BF339448 602039102
32	538.8	42.5	867	13	BX326018		BX326018 BX326018
33	535	42.2	778	13	BU750981		BU750981 CH3#037_B
34	531.2	41.9	894	13	BX408562		BX408562 BX408562
35	530.4	41.8	644	12	BG938621		BG938621 cn27c11.x
36	482.2	38.0	627	12	BI183862		BI183862 UNL-P-FN-
c 37	481.4	37.9	627	10	BF090699		BF090699 QV2-NT004
38	472.4	37.2	933	13	BQ716088		BQ716088 AGENCOURT
39	470	37.0	912	12	BI768516		BI768516 603057118
40	462.4	36.4	803	13	BU356104		BU356104 603476062
41	462	36.4	462	10	BE656312		BE656312 UI-M-BH0-
42	460.6	36.3	882	12	BI825121		BI825121 603038662
43	454.8	35.8	576	9	AW142226		AW142226 EST292462
44	452	35.6	1022	13	BU150258		BU150258 AGENCOURT
45	449.8	35.4	745	10	BG431026		BG431026 602498636